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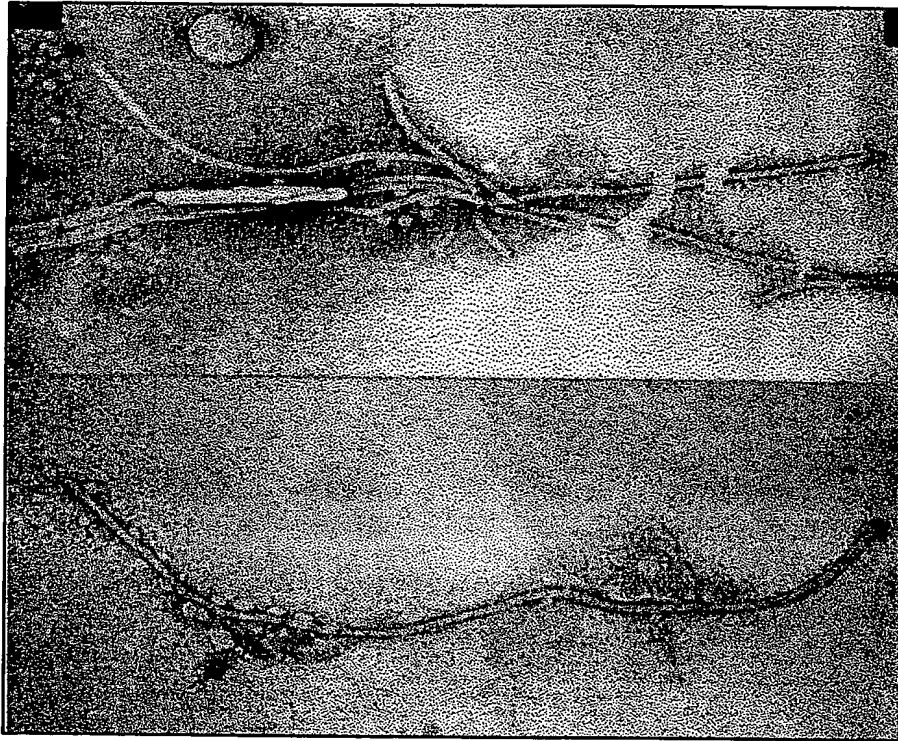
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***FIG. 1***

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TGTGGACAGCAATCTTCCAAAGAAAGACAGGGATGACATCATGGAAGCGAGTCGACGACT  
1 ----- (93-110) -----+-----+-----+-----+-----+-----+ 60  
ACACCTGTCGTTAGAAGGTTTCTTTCTGTCCCTACTGTAGTACCTTCGCTCAGCTGCTGA  
V D S N L P K K D R D D I M E A S R R L -  
  
ATCGCCATCGGACGCCGCCTTTTGCAGAGCAGTGTCCGTTTCAGGTAGGGAAGTATGTGGA  
61 -----+-----+-----+-----+-----+-----+ 120  
TAGCGGTAGCCTGCGGCGGAAAACGTCTCGTCACAGCCAAGTCCATCCCTTCATACACCT  
S P S D A A F C R A V S V Q V G K Y V D -  
  
CGTAACGCAGAATTTAGAAAGTACGATCGTGCCGTTAAGAGTTATGGAAATAAGAAAAG  
121 ----- (93-25) -----+-----+-----+-----+-----+ 180  
GCATTGCGTCTTAAATCTTTTCATGCTAGCACGGCAATTCTCAATACCTTTATTTCTTTTC  
V T Q N L E S T I V P L R V M E I K K R -  
  
ACGAGGATCAGCACATGTTAGTTTACCGAAGGTGGTATCCGCTTACGTAGATTTTTTATAC  
181 -----+-----+-----+-----+-----+-----+ 240  
TGCTCCTAGTCGTGTACAATCAAATGGCTTCCACCATAGGCGAATGCATCTAAAAATATG  
R G S A H V S L P K V V S A Y V D F Y T -  
  
GAACTTGCAGGAATTGCTGTCCGATGAAGTAACTAGGGCCAGAACCGATACAGTTTTCGGC  
241 -----+-----+-----+-----+-----+-----+ 300  
CTTGAACGTCCTTAACGACAGCCTACTTTCATTGATCCCGGTCTTGGCTATGTCAAAGCCG  
N L Q E L L S D E V T R A R T D T V S A -  
  
ATACGCTACCGACTCTATGGCTTTCTTAGTTAAGATGTTACCCCTGACTGCTCGTGAGCA  
301 -----+-----+-----+-----+----- (93-40) -----+ 360  
TATGCGATGGCTGAGATACCGAAAGAATCAATTCTACAATGGGGACTGACGAGCACTCGT  
Y A T D S M A F L V K M L P L T A R E Q -  
  
GTGGTTAAAAGACGTGCTAGGATATCTGCTAGTACGGAGACGACCAGCAAATTTTTCTTA  
361 -----+-----+-----+-----+-----+-----+ 420  
CACCAATTTTTCTGCACGATCCTATAGACGATCATGCCTCTGCTGGTCGTTTAAAAGGAT  
W L K D V L G Y L L V R R R P A N F S Y -  
  
CGACGTAAGAGTAGCTTGGGTATATGACGTGATCGCTACGCTCAAGCTGGTCATAAGATT  
421 -----+-----+-----+-----+-----+-----+ 480  
GCTGCATTCTCATCGAACCCATATACTGCACTAGCGATGCGAGTTCGACCAGTATTCTAA  
D V R V A W V Y D V I A T L K L V I R L -  
  
GTTTTTCAACAAGGACACACCCGGGGGTATTAAAGACTTAAACCGTGTGTGCCTATAGA  
481 -----+-----+-----+-----+-----+-----+ 540  
CAAAAAGTTGTTCTGTGTGGGCCCCCATAATTTCTGAATTTTGGCACACACGGATATCT  
F F N K D T P G G I K D L K P C V P I E -  
  
GTCATTGACCCCTTTCACGAGCTTTTCGTCCTATTTCTCTAGGTTAAGTTACGAGATGAC  
541 -----+-----+-----+-----+-----+-----+ 600  
CAGTAAGCTGGGGAAAGTGCTCGAAAGCAGGATAAAGAGATCCAATTCAATGCTCTACTG  
S F D P F H E L S S Y F S R L S Y E M T -  
  
GACAGGTAAAGGGGGAAAGATATGCCCCGAGATCGCCGAGAAGTTGGT  
601 -----+-----+-----+-----+----- (92-98) ----- 648  
CTGTCCATTTCCCCCTTTCTATACGGGCCTCTAGCGGCTCTTCAACCA  
T G K G G K I C P E I A E K L -

FIG. 2

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BYV\_p64 115\_VGCKFNIQSVTEFVKKINGNVAEPSLVEHCWSLSNSCGELINPKDTKRFV  
CTV\_p61 108\_VGCRFTLNDVESYLMRGEDEFADLAAVEHSWCLSNSCSRLLSSTEIDANK  
LIYV\_P59 131\_EGCSFTEQQVVEKYPQVDSLVAKIL.....YRVCNSLGLKLLDLKDFENKN  
GLRaV3\_p55 114\_VDSNLPKKDRDDIME..ASRRLSPSDAAFCRAVSVQVGKYVDVTQNLEST

CONSENSUS vgc-f----v-e-----a-----w--sns-g-l----d-----

BYV\_p64 SLIFKGKDLAESTDEAIVS..SSYLDYLSHCLNLYETCNLSSNSGKKSLY  
CTV\_p61 TLVF.TKNFDSNISG..VT..TKLETYLSYCISLYKKHCM.KDDDYFNLI  
LIYV\_P59 ISGFEINTAQDSPTVADDN..ES.NDFFRECVDNQRYYSLSGSKLGKAK  
GLRaV3\_p55 IVPLRVMEIKKRRGSAHVSLPKVVSAYVDFYTNLQELLSDEVTRARTDTV

CONSENSUS ---f-----a-v-----yl--c-nl-----

BYV\_p64 DEFLKHVIDYL...ENS DLEYRSPSDNPLVAGILYDMCFEYNTLKSTYLK  
CTV\_p61 LPMFNCLMKVL...ASLGLFYEKHADNPLLTGMLIEFCLENKVYYSTFKV  
LIYV\_P59 LEANAYIFKILLKSASGEFDIDRLSRNPLAISKF MNLYTNHVTDSETFKS  
GLRaV3\_p55 SAYATDSMAFLVKMLPLT.....AREQWLKDVLGYLLVRRR PANFSYDV

CONSENSUS -----L-----l-----npl----l--lc-----t---

BYV\_p64 NIESFDCFLSLYLPLLSEVFSMNWERPAPDVRLLFELDAAELLLKVPTIN  
CTV\_p61 NLDNVRLFKSKVLPVLTVDI SEPDDPVDERVLIPFDPTDFVLDLPKLN  
LIYV\_P59 KFEALKSIKTPFASF IKKAFGIR.....LNFEDSKIFYALPKER  
GLRaV3\_p55 RVAWVYDVIATLKL VIRLFFNKDTPGGIKDLKPCVP IESFDPFHELS...

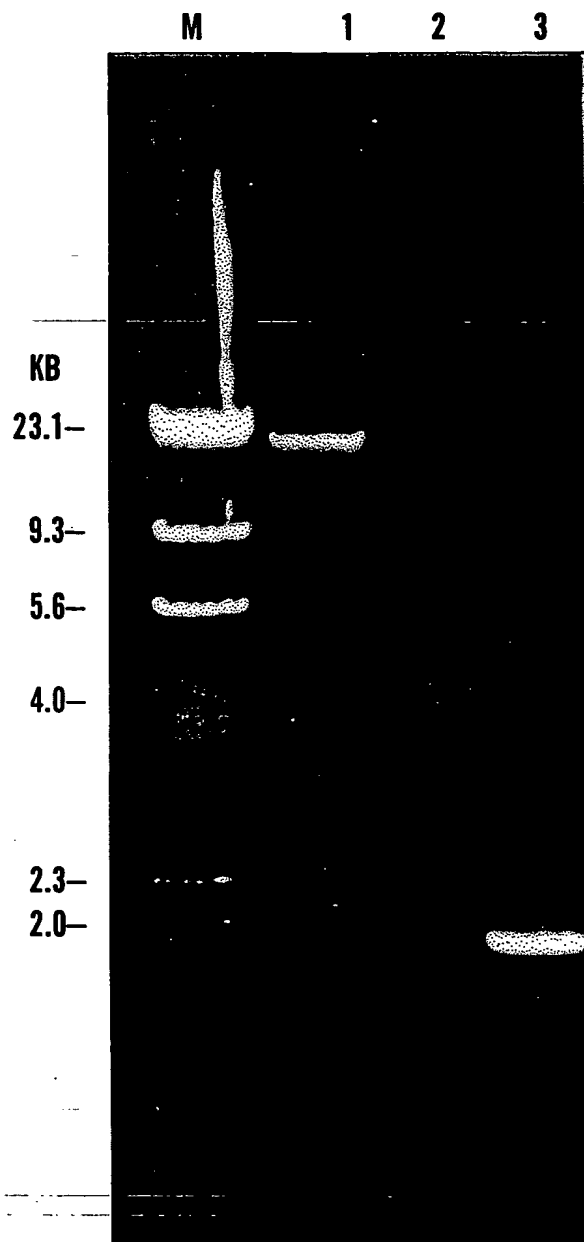
CONSENSUS --e-----i--f-----d-----f--d-f--lp---

BYV\_p64 MHDST...FLYKNKLRYLESYFEDDSNELIKVKVDSLL  
CTV\_p61 IHDTM...VVVG NQIRQLEYVVESDALDDLSQHVDLRL  
LIYV\_P59 QSDVLSDDMMVESIVRDAASFTTVSDNNYLP ERVDRFV  
GLRaV3\_p55 .....SYFSRLSYEMTTGKGKICPEIAEKL

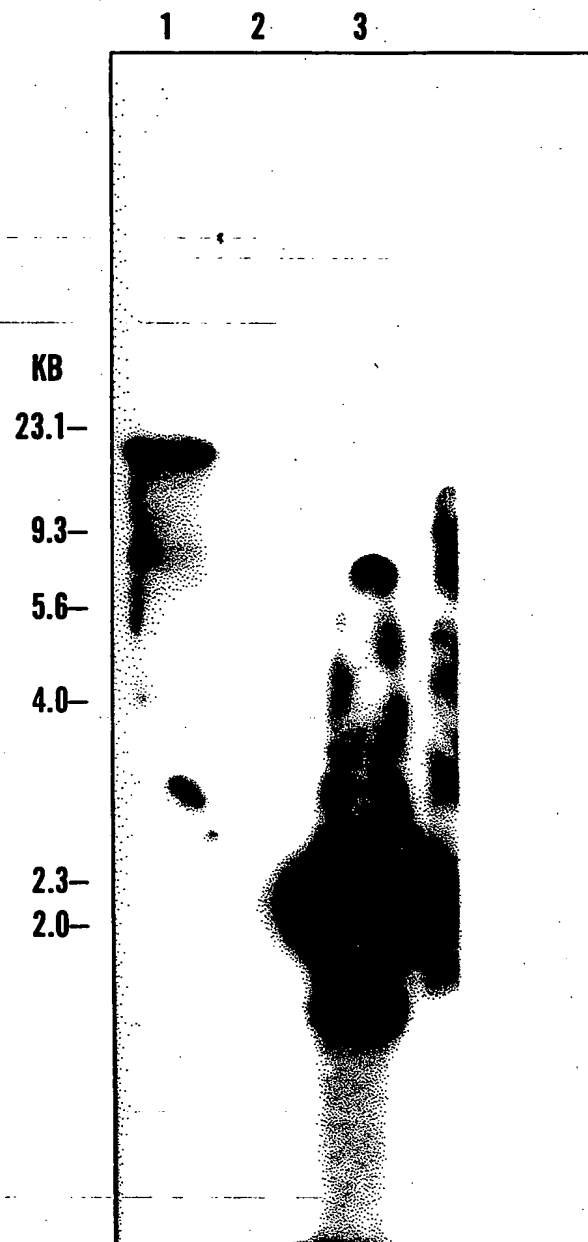
CONSENSUS --d-----r-l-----vd--l

**FIG. 3**

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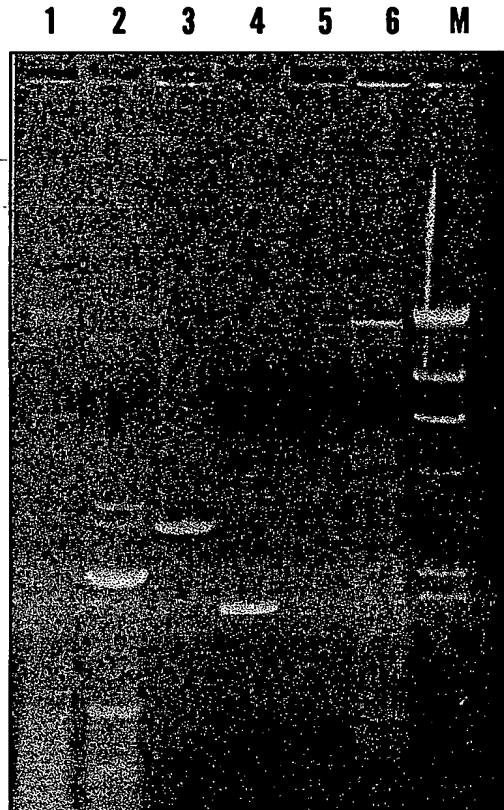


**FIG. 4A**



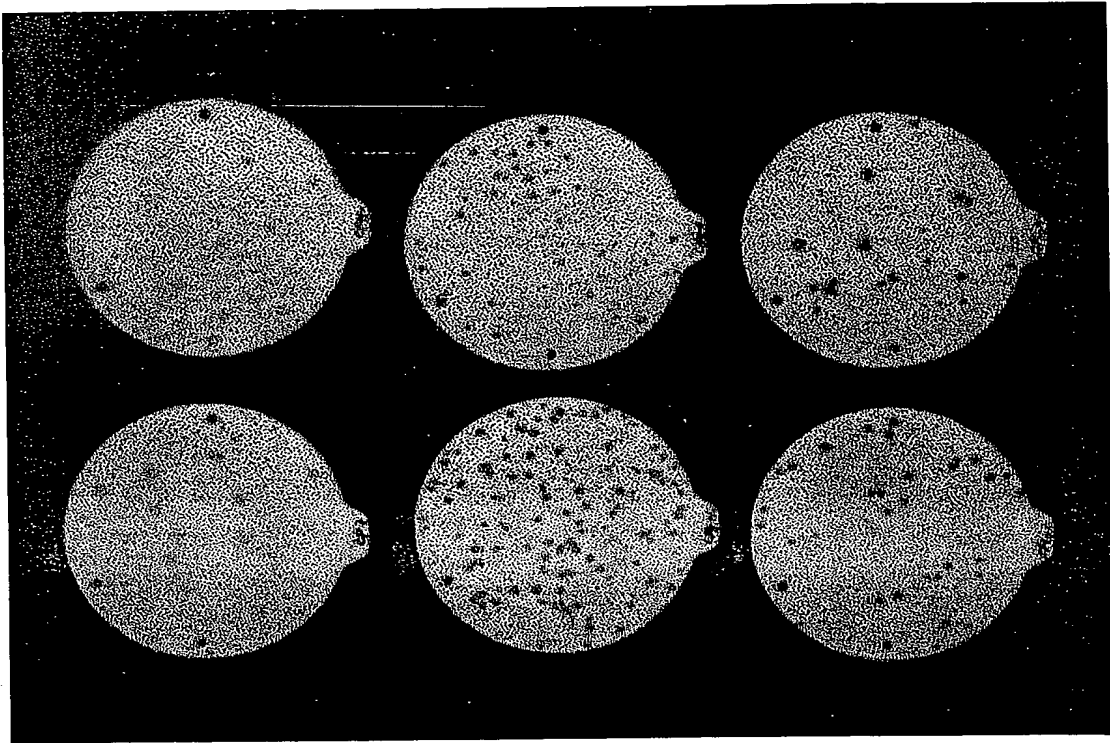
**FIG. 4B**

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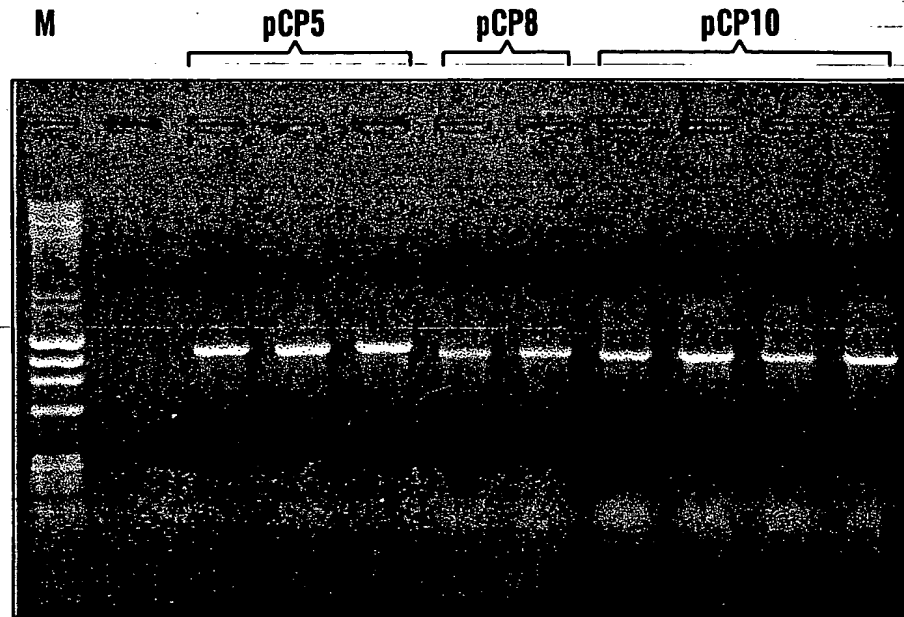
***FIG. 5***

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***FIG. 6***

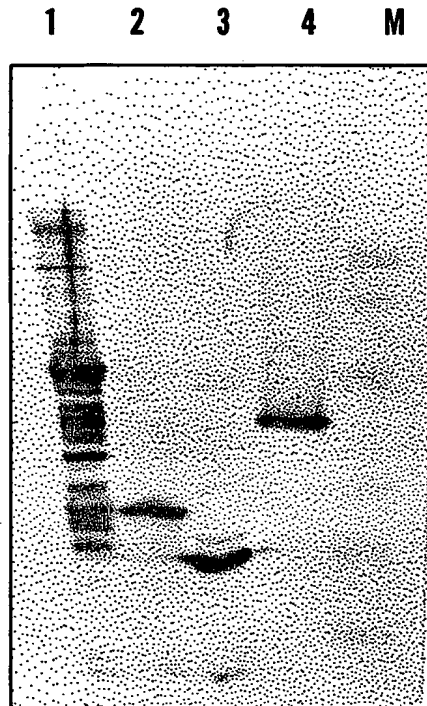
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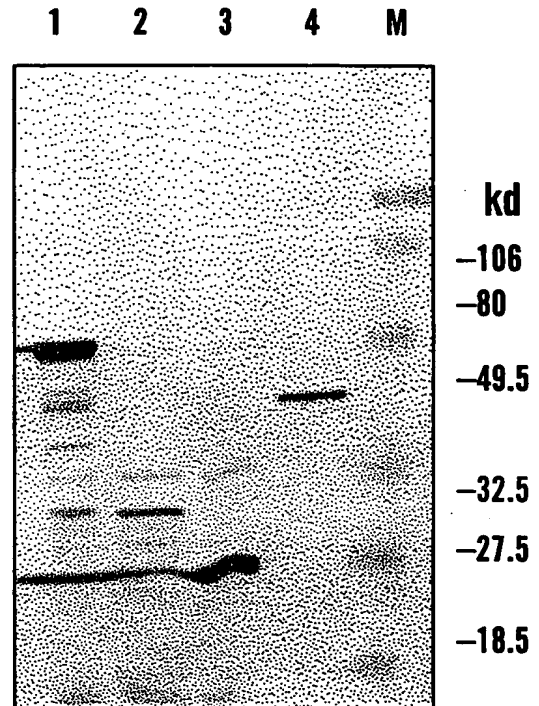
***FIG. 7***



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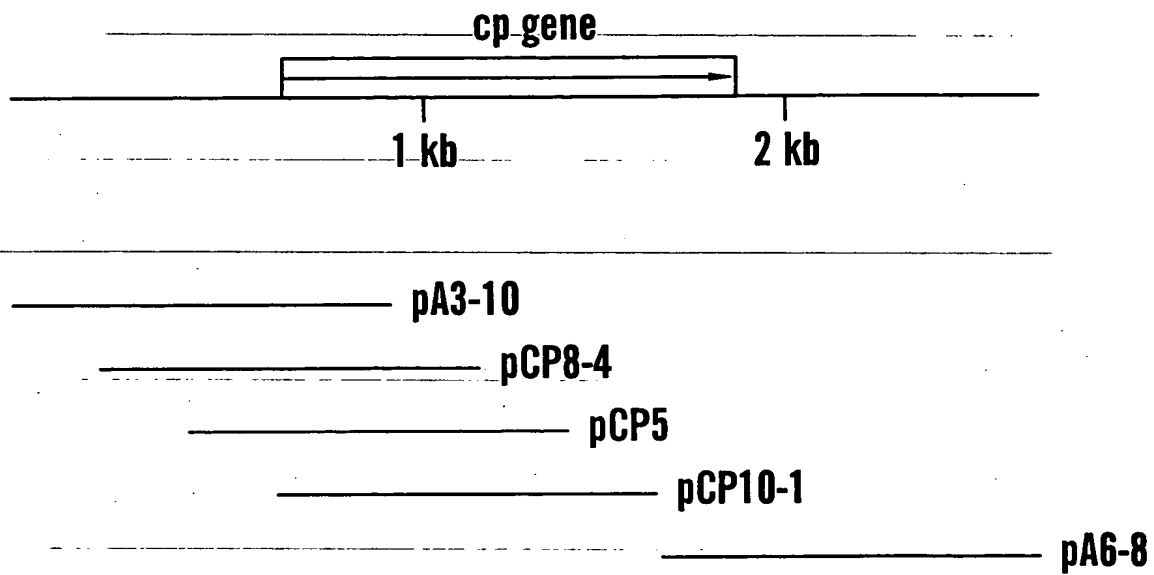


**FIG. 8A**



**FIG. 8B**

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**FIG. 9**

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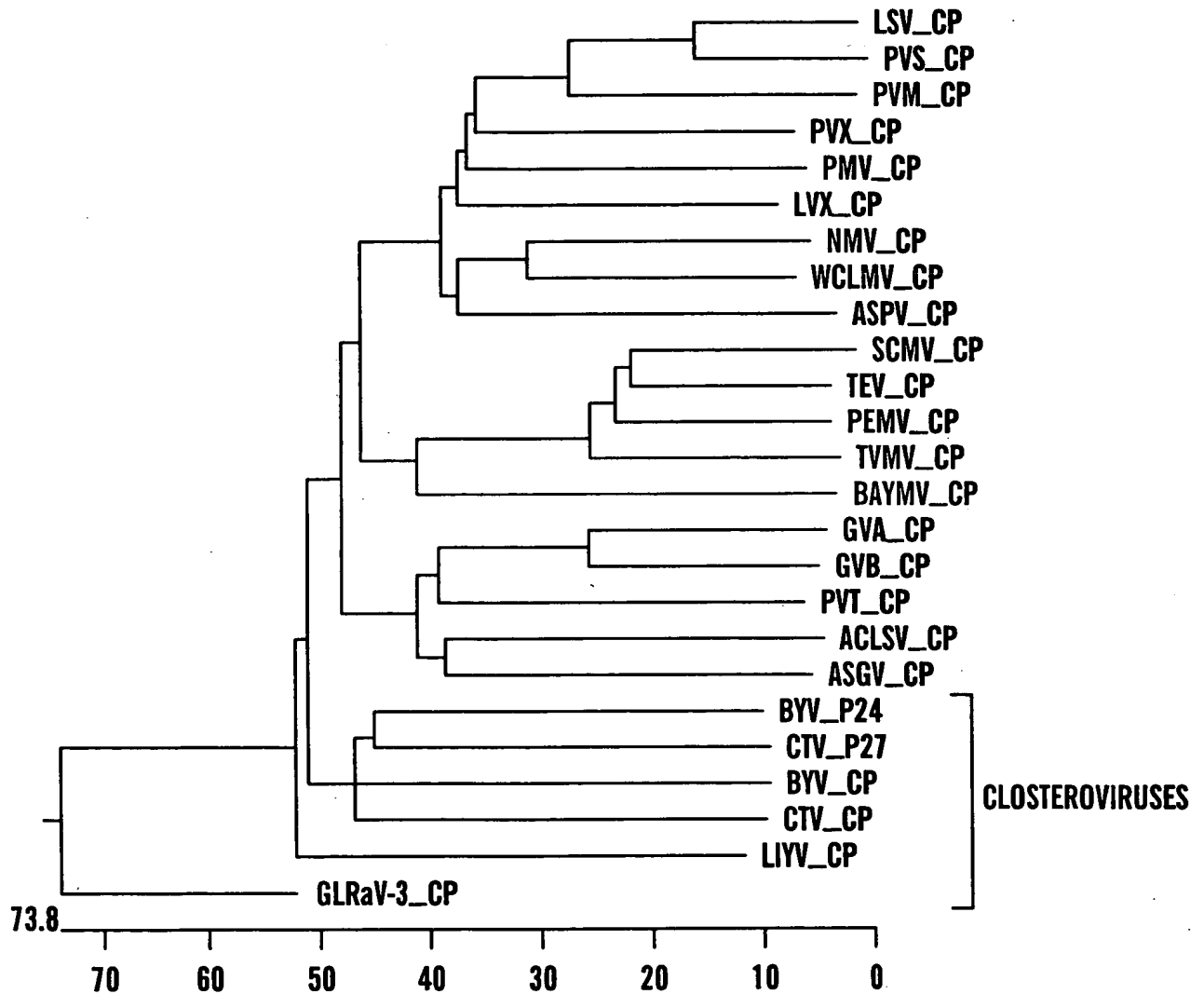
```
1  ATGGCATTGTGAAC TGAAT TAGGGCAGATATATGAAGTCGTCCCCGAAAATAATTTGAGA 60
  M A F E L K L G Q I Y E V V P E N N L R -
61  GTTAGAGTGGGGGATGCGGCACAAGGAAAATTTAGTAAGGCGAGTTTCTTAAAGTACGTT 120
  V R V G D A A Q G K F S K A S F L K Y V -
121 AAGGACGGGACACAGGCGGAATTAACGGGAATCGCCGTAGTGCCCGAAAAATACGTATTC 180
  K D G T Q A E L T G I A V V P E K Y V F -
181 GCCACAGCAGCTTTGGCTACAGCGGCGCAGGAGCCACCTAGGCAGCCACCAGCGCAAGTG 240
  A T A A L A T A A Q E P P R Q P P A Q V -
241 GCGGAACCACAGGAAACCGATATAGGGGTAGTGCCGGAATCTGAGACTCTCACACCAAAT 300
  A E P Q E T D I G V V P E S E T L T P N -
301 AAGTTGGTTTTCGAGAAAGATCCAGACAAGTTCTTGAAGACTATGGGCAAGGGAATAGCT 360
  K L V F E K D P D K F L K T M G K G I A -
361 TTGGACTTGGCGGGAGTTACCCACAAACCGAAAGTTATTAACGAGCCAGGGAAAGTATCA 420
  L D L A G V T H K P K V I N E P G K V S -
421 GTAGAGGTGGCAATGAAGATTAATGCCGCATTGATGGAGCTGTGTAAGAAGGTTATGGGC 480
  V E V A M K I N A A L M E L C K K V M G -
481 GCCGATGACGCAGCAACTAAGACAAAATTCTTCTTGTACGTGATGCAGATTGCTTGCACG 540
  A D D A A T K T K F F L Y V M Q I A C T -
541 TTCTTTACATCGTCTTCGACGGAGTTCAAAGAGTTTGA CTACATAGAAACCGATGATGGA 600
  F F T S S S T E F K E F D Y I E T D D G -
601 AAGAAGATATATGCGGTGTGGGTATATGATTGCATTAAACAAGCTGCTGCTTCGACGGGT 660
  K K I Y A V W V Y D C I K Q A A A S T G -
661 TATGAAAACCCGGTAAGGCAGTATCTAGCGTACTTCACACCAACCTTCATCAGGGCGACC 720
  Y E N P V R Q Y L A Y F T P T F I T A T -
721 CTGAATGGTAAACTAGTGATGAACGAGAAGGTTATGGCACAGCATGGAGTACCACCGAAA 780
  L N G K L V M N E K V M A Q H G V P P K -
781 TTCTTTCCGTACACGATAGACTGCGTTCGTCCGACGTACGATCTGTTCAACAACGACGCA 840
  F F P Y T I D C V R P T Y D L F N N D A -
841 ATATTAGCATGGAATTTAGCTAGACAGCAGGCGTTTAGAAACAAGACGGTAACGGCCGAT 900
  I L A W N L A R Q Q A F R N K T V T A D -
901 AACACCTTACACAACGTCTTCCA ACTATTGCAAAAGAAGTAG 942
  N T L H N V F Q L L Q K K *
```

FIG. 10

	1				50
BYV_CP	.....	.....	.....	.....	.....
CTV_CP	.....	.....	.....	.....	.....
LIYV_CP	.....	.....	.....	.....	.....
GLRaV3_CP	MAFELKLGQI	YEVVPENNLR	VRVGDAAQGK	FSKASFLKYV	KDGTQAEALTG
CONSENSUS	-----	-----	-----	-----	-----
	51				100
BYV_CP	.....	.....	.....	.....	.....
CTV_CP	.....	.....	.....	.....	MDDETKKLKN
LIYV_CP	.....	MDTDGD	NDVFGSGNDT	RNNDDKKKEE	MKQNISDNSQ
GLRaV3_CP	IAVVPEKYVF	ATAALATAAQ	EPPRQPPAQV	AEPQETDIGV	VPESETLTPN
CONSENSUS	-----	-----	-----	-----	-----
	101				150
BYV_CP	....MGSAE	PISAIA..TF	ENVSL.AD.Q	TCLHGEDCDK	LRK.....N
CTV_CP	KNKETKEGDD	VVAAES..SF	GSVNLHID.P	TLITMNDVRQ	LSTQQNAALN
LIYV_CP	IISTRDHEAD	IIGSISKEDL	SKIVVRVDRH	DALSANDVQS	FR...EAMIN
GLRaV3_CP	KLVFEKDPDK	FLKTMGKGIA	LDLAGVTHKP	KVI..NEPGK	VSVEVAMKIN
CONSENSUS	-----d	-i-----f	--v----d--	-----nd---	1-----N
	151				200
BYV_CP	FEECLKLKG.	...VPEDNLG	IALGLCLYSC	AT.IGTSNKV	NVQPTS.TFI
CTV_CP	RDLFLALKGK	YPNLPDKDKD	FHIAMMLYRL	AV.KSSSLQS	DDDTTGITYT
LIYV_CP	...FMRDKDP	NRNQPSDKLI	IAMEVGVIQM	VINLGTSAKL	G.NANNLEFT
GLRaV3_CP	.AALMELCKK	VMGADDAATK	TKFFLYVMQI	ACTFFTS..S	STEFKEFDYI
CONSENSUS	---f--lk--	----pd----	----l--y--	a----ts---	-----
	201				250
BYV_CP	KASFGGGKEL	YLTHGELNSF	LGSQKLLEGK	PNKLRCFCRT	FQKDYISLRK
CTV_CP	R....EGVEV	DLSDKLWTDI	VYNSKGIGNR	TNALRVWGRT	NDALYLAFCR
LIYV_CP	IAYDQETR TY	KVAD..FVNY	MQSR..MRNS	PNVVRQYARA	MEKTINNIRS
GLRaV3_CP	ET..DDGKKI	Y..AVWVYDC	IKQAAASTGY	ENPVRQYLAY	FTPFTITATL
CONSENSUS	-----eg---	-----	-----	-N--R-y-r-	----y-----
	251				300
BYV_CP	EYRGKLPPIA	RANRHGLPAE	DHYLAADF.I	STSTELTDLQ	QSRLLLAREN
CTV_CP	QNR.NLSYGG	RPLDAGIPAG	YHYLCADF.L	.TGAGLTDLE	CAVYIQAKEQ
LIYV_CP	AGIIN.SNGV	LAAKHGVLAS	YRNSYSDFAV	GFGNDTTDAQ	LTSMLLARKQ
GLRaV3_CP	NGKLVMEKV	MA.QHGVPPK	FFPYTIDCVR	PTYDLFNDA	ILAWNLARQQ
CONSENSUS	-----l----	-a--hGvpa-	y-----Df--	-t---ltd--	-----lAr-q
	301				328
BYV_CP	ATH.TEFSSE	SPVTSCLKQLG	RGLGTGR*		
CTV_CP	LLK.KRGAD	VVVTNVRQLG	K.FNTR*.		
LIYV_CP	ALC.KGEGGS	VEHYNTMQLA	NLKHPC*.		
GLRaV3_CP	AFRNKTVTAD	NTLHNVFQLL	QKK*....		
CONSENSUS	al--k----e	----n--QL-	-----		

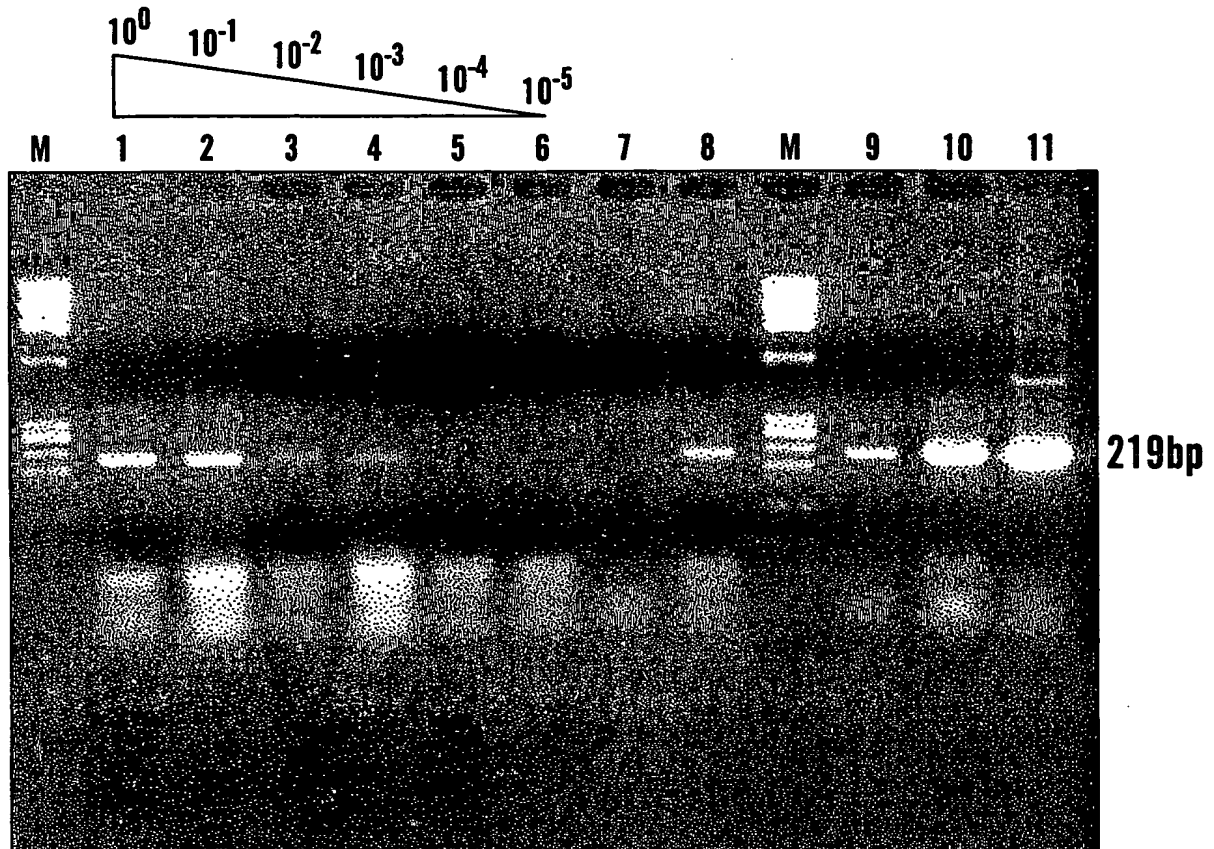
**FIG. 11**

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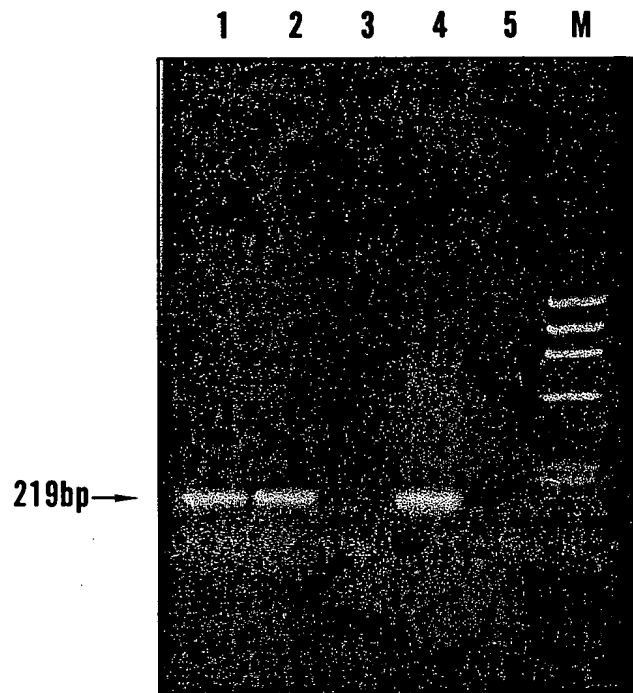
**FIG. 12**

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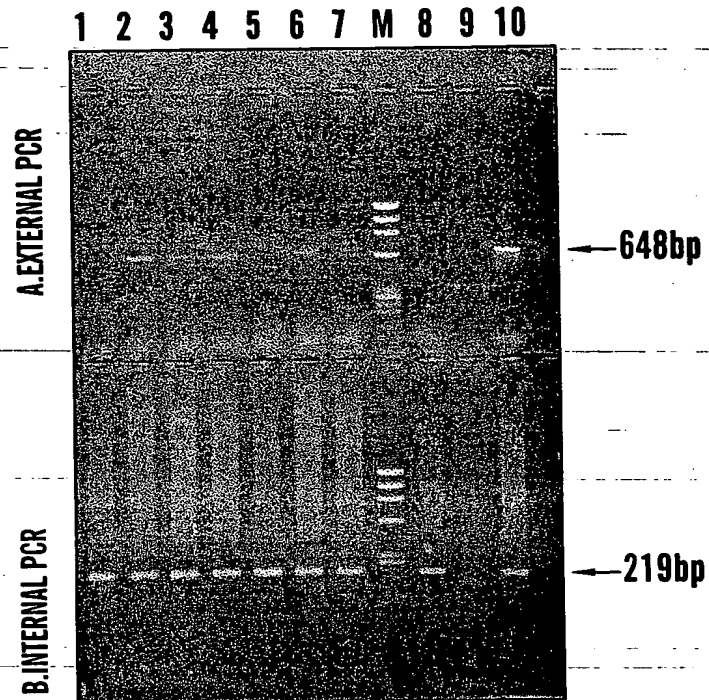
**FIG. 13**

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**FIG. 14**

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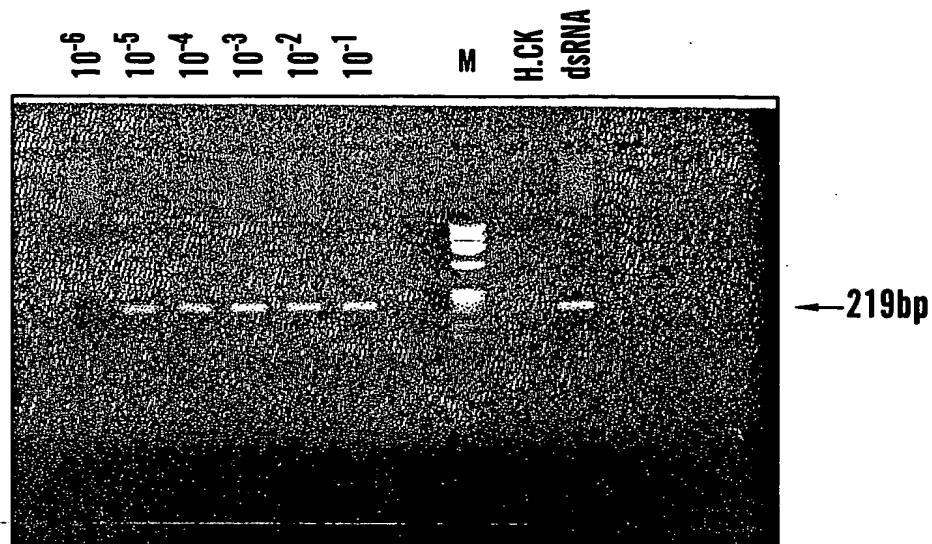


**FIG. 15**



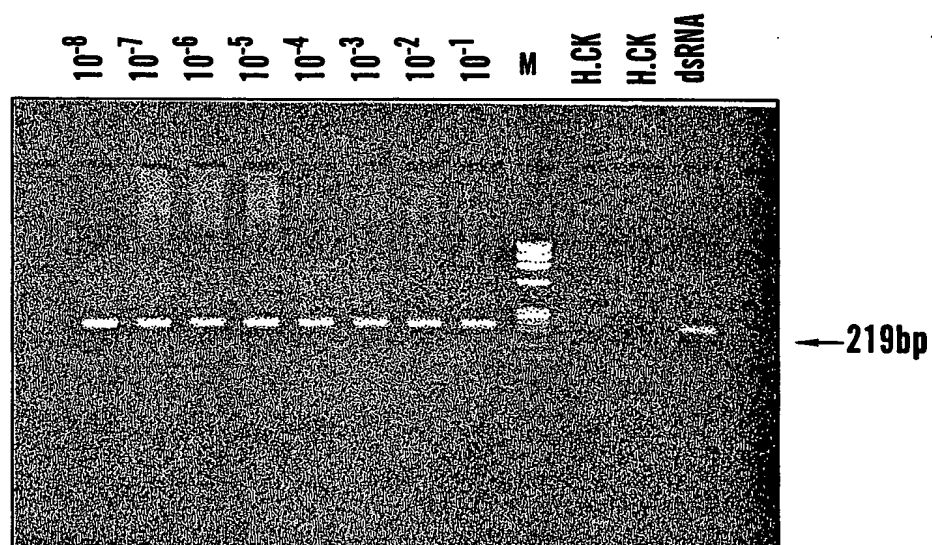
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A. PK NESTED PCR



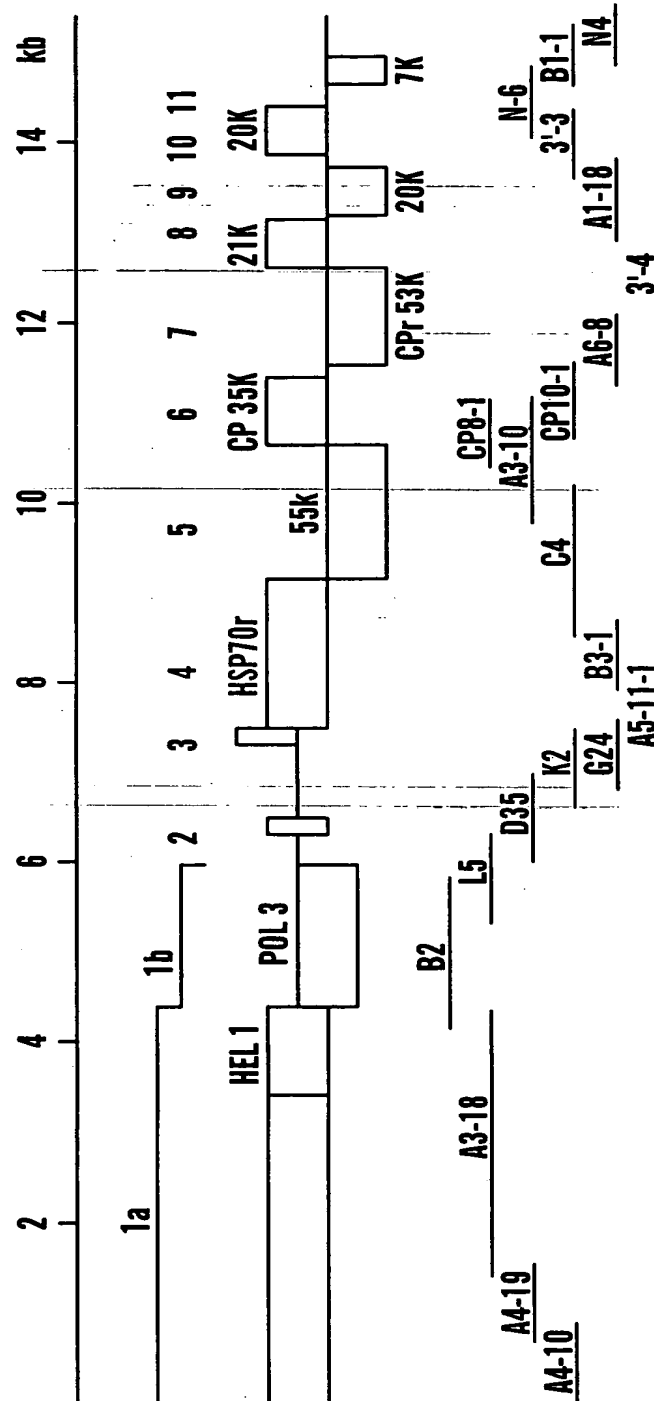
**FIG. 16A**

B. IC NESTED PCR



**FIG. 16B**

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**FIG. 17**

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FIG. 18A

ORF1a (HELICASE)

GTGTCTACTTACGCGAAGAGTGTGATGAACGACAATTTCAATATCCTTGAGACCCTGGTA  
1 -----+-----+-----+-----+-----+-----+ 60  
CACAGATGAATGCGCTTCTCACTACTTGCTGTTAAAGTTATAGGAACTCTGGGACCAT  
a V S T Y A K S V M N D N F N I L E T L V -  
  
ACTTTGCCCAAGTCCTTTATAGTCAAAGTACCTGGTTCGGTGCTGGTTAGCATAACCACT  
61 -----+-----+-----+-----+-----+-----+ 120  
TGAAACGGGTTTCAGGAAATATCAGTTTCATGGACCAAGCCACGACCAATCGTATTGGTGA  
a T L P K S F I V K V P G S V L V S I T T -  
  
TCGGGCATTTCCGACAACTTGAAGTTCGGGGCGCGTTCGACGTTTCTAAAAAGAATTTCT  
121 -----+-----+-----+-----+-----+-----+ 180  
AGCCCGTAAAGGCTGTTTGAAGTTCGAGCCCGCGCAAGCTGCAAGATTTTCTTAAAG  
a S G I S D K L E L R G A F D V S K K N F -  
  
TCCAGGAGGTTACGTTTCGAGTCGTTTGCGCGTATTTTCTAGGGCTATTGTGGAGGATACG  
181 -----+-----+-----+-----+-----+-----+ 240  
AGGTCCTCCAATGCAAGCTCAGCAAACGCGCATAAAGATCCCGATAACACCTCCTATGC  
a S R R L R S S R L R V F S R A I V E D T -  
  
ATCAAGGTTATGAAGGGCATGAAATCAGAGGATGGTAAACCACTCCCTATAGCCGAGGAT  
241 -----+-----+-----+-----+-----+-----+ 300  
TAGTTCCAATACTTCCCGTACTTTAGTCTCCTACCATTGTTGGTGAGGGATATCGGCTCCTA  
a I K V M K G M K S E D G K P L P I A E D -  
  
TCCGTGTACGCGTTCATGACAGGCAATATGTCAAACGTTTCATTGCACTAGGGCTGGTTTG  
301 -----+-----+-----+-----+-----+-----+ 360  
AGGCACATGCGCAAGTACTGTCCGTTTATACAGTTTGCAAGTAACGTGATCCCGACCAAAC  
a S V Y A F M T G N M S N V H C T R A G L -  
  
CTCGGGGGCTCAAAGGCTTGCGCGGCTTCTTTAGCTGTGAAGGGTGCAGCTTCACGCGCT  
361 -----+-----+-----+-----+-----+-----+ 420  
GAGCCCCCGAGTTTCCGAACGCGCCGAAGAAATCGACACTTCCCACGTGCAAGTGCGCGA  
a L G G S K A C A A S L A V K G A A S R A -  
  
ACTGGAACAAACTCTTTTCAGGTCTCACATCCTTTCTTTCCGCCGGTGGTCTGTTTTAC  
421 -----+-----+-----+-----+-----+-----+ 480  
TGACCTTGTTTTGAGAAAAGTCCAGAGTGTAGGAAAGAAAGGCGGCCACCAGACAAAATG  
a T G T K L F S G L T S F L S A G G L F Y -  
  
GATGAAGGCTTGACGCCCCGAGAGAGGCTTGATGCACTAACGCGCCGTGAACATGCTGTG  
481 -----+-----+-----+-----+-----+-----+ 540  
CTACTTCCGAAGTGGGGCTCTCTCCGAAGTACGTGATTGCGCGGCACTTGTACGACAC  
a D E G L T P G E R L D A L T R R E H A V -  
  
AATTCACCTGTAGGCCTCTTAGAACCTGGAGCTTCGGTTGCGAAGCGGGTTCGTTTCCGGA  
541 -----+-----+-----+-----+-----+-----+ 600  
TTAAGTGGACATCCGGAATCTTGGACCTCGAAGCCAACGCTTCGCCCAGCAAAGGCCT  
a N S P V G L L E P G A S V A K R V V S G -  
  
ACGAAAGCTTTTCTGTCAGAATTGTCATTGGAGGACTTCACCACTTTTCGTCATAAAAAAT  
601 -----+-----+-----+-----+-----+-----+ 660  
TGCTTTCGAAAAGACAGTCTTAACAGTAACCTCCTGAAGTGGTGAAAGCAGTATTTTAA  
a T K A F L S E L S L E D F T T F V I K N -

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**FIG. 18B**

```
AGGGTGCTTATTGGTGTGTTTTACTCTTTCCATGGCTCTCACTCCGGTGGTCTGGAAGTAC
661 -----+-----+-----+-----+-----+-----+-----+ 720
TCCCACGAATAACCACAAAATGAGAAAGGTACCGAGAGTGAGGCCACCAGACCTTCATG
a R V L I G V F T L S M A L T P V V W K Y -

AGAAGGAATATCGCGCGAACTGGCGTGATGTTTTCCACCGTGCTCGTTCCGGTACCGCG
721 -----+-----+-----+-----+-----+-----+-----+ 780
TCTTCCTTATAGCGCGCTTGACCGCACCTACAAAAGGTGGCAGCAGCAAGCCCATGGCGC
a R R N I A R T G V D V F H R A R S G T A -

GCCATCGGTTTACAATGTCTTAGTGAGGAAGGTCGTTAGCTGGTGACGCTGCTCGTGGC
781 -----+-----+-----+-----+-----+-----+-----+ 840
CGGTAGCCAAATGTTACAGAATCACCTCCTTCCAGCAATCGACCACTGCGACGAGCACCG
a A I G L Q C L S G G R S L A G D A A R G -

GCGTTAACAGTGA CTGAGGAGGGCTATCTTCGGCGGTTGCGGTGACCAGAAATACAGTG
841 -----+-----+-----+-----+-----+-----+-----+ 900
CGCAATTGTCACTGAGCTCCTCCCGATAGAAGCCGCCAACGCCACTGGTCTTTATGTCAC
a A L T V T R G G L S S A V A V T R N T V -

GCTAGGCGTCAGGTACCATTGGCGTGTCTTTTCGTTTTCCACGTCTTACGCAGTCAGTGGT
901 -----+-----+-----+-----+-----+-----+-----+ 960
CGATCCGCAGTCCATGGTAACCGCAACGAAAGCAAAAGGTGCAGAATGCGTCAGTCACCA
a A R R Q V P L A L L S F S T S Y A V S G -

TGCACTTTGTTAGGTATTTGGGCTCATGCTCTCCCTAGGCATTTGATGTTCTTCTTTGGC
961 -----+-----+-----+-----+-----+-----+-----+ 1020
ACGTGAAACAATCCATAAACCCGAGTACGAGAGGGATCCGTAAACTACAAGAAGAAACCG
a C T L L G I W A H A L P R H L M F F F G -

CTAGGGACGCTCTTCGGGGTGAGTGCCAGTACCAATTCTTGGTCGCTTGGGGGCTATACG
1021 -----+-----+-----+-----+-----+-----+-----+ 1080
GATCCCTGCGAGAAGCCCCACTCACGGTCATGGTTAAGAACCAGCGAACCCCCGATATGC
a L G T L F G V S A S T N S W S L G G Y T -

AACAGTCTGTTACCGTACCGGAATTAAGTTGGGAAGGAGGAGTTACAGATCTTTATTG
1081 -----+-----+-----+-----+-----+-----+-----+ 1140
TTGTCAGACAAGTGGCATGGCCTTAATTGAACCTTCCCTCCTCAATGTCTAGAAATAAC
a N S L F T V P E L T W E G R S Y R S L L -

CCCCAAGCAGCTTTAGGTATTTCTCTCGTTGTGCGCGGGTGTGTTAAGTGAAACTGTGCCA
1141 -----+-----+-----+-----+-----+-----+-----+ 1200
GGGGTTCGTCGAAATCCATAAAGAGAGCAACACGCGCCCAACAATTCACCTTTGACACGGT
a P Q A A L G I S L V V R G L L S E T V P -

CAACTAACGTACGTACCGCCGATTGAAGGTCCGAATGTTTATGATCAGGCACTAAATTTT
1201 -----+-----+-----+-----+-----+-----+-----+ 1260
GTTGATTGCATGCATGGCGGCTAACTTCCAGCCTTACAAATACTAGTCCGTGATTTAAAA
a Q L T Y V P P I E G R N V Y D Q A L N F -

TATCGCGACTTTGACTATGACGATGGTGCAGGCCCATCCGGGACGGCTGGTCAAAGCGAT
1261 -----+-----+-----+-----+-----+-----+-----+ 1320
ATAGCGCTGAAACTGATACTGCTACCACGTCCGGGTAGGCCCTGCCGACCAGTTTCGCTA
a Y R D F D Y D D G A G P S G T A G Q S D -
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**FIG. 18C**

1321 CCTGGAACCAATACTTCGGATACTTCTTCGGTTTTCTCTGACGATGGTTTGCCCGCTAGT  
-----+-----+-----+-----+-----+-----+ 1380  
GGACCTTGGTTATGAAGCCTATGAAGAAGCCAAAAGAGACTGCTACCAAACGGGCGATCA  
a P G T N T S D T S S V F S D D G L P A S -

1381 GGCGGTGGCTTCGACGCGCGCGTTGAGGCAGGTCCCAGCCATGCTGTTGATGAATCACCA  
-----+-----+-----+-----+-----+-----+ 1440  
a CCGCCACCGAAGCTGCGCGCGCAACTCCGTCCAGGGTCGGTACGACAACCTACTTAGTGGT  
G G G F D A R V E A G P S H A V D E S P -

1441 AGGGGTAGTGTGAGTTCGTCTACAGAGAACGTGTAGATGAACATCCGGCGTGTGGTGAA  
-----+-----+-----+-----+-----+-----+ 1500  
a TCCCCATCACAACCTCAAGCAGATGTCTCTTGACATCTACTTGTAGGCCGCACACCACTT  
R G S V E F V Y R E R V D E H P A C G E -

1501 GCTGAAGTTGAAAAGGATCTAATAACACCACTTGGTACAGCTGTCTTAGAGTCGCCCCC  
-----+-----+-----+-----+-----+-----+ 1560  
a CGACTTCAACTTTTCCTAGATTATTGTGGTGAACCATGTTCGACAGAATCTCAGCGGGGGG  
A E V E K D L I T P L G T A V L E S P P -

1561 GTAGGTCCTGAAGCTGGGAGCGCGCCCAACGTCGAGGACGGTTGTCCGGAGGTTGAAGCT  
-----+-----+-----+-----+-----+-----+ 1620  
a CATCCAGGACTTCGACCCTCGCGCGGGTTGCAGCTCCTGCCAACAGGCCTCCAACCTCGA  
V G P E A G S A P N V E D G C P E V E A -

1621 GAGAAATGTTTCGGAGGTCATCGTTGACGTTCCCTAGTTCAGAACCGCCGGTACAAGAAGTC  
-----+-----+-----+-----+-----+-----+ 1680  
a CTCTTTACAAGCCTCCAGTAGCAACTGCAAGGATCAAGTCTTGGCGGCCATGTTCTTCAG  
E K C S E V I V D V P S S E P P V Q E V -

1681 CTTGAATCAACCAATGGTGTCCAAGCTGCAAGAACTGAAGAGGTGTGTCAGGGCGACACA  
-----+-----+-----+-----+-----+-----+ 1740  
a GAACTTAGTTGGTTACCACAGGTTTCGACGTTCTTGAAGTCTTCCAACACGTCCCGCTGTGT  
L E S T N G V Q A A R T E E V V Q G D T -

1741 TGTGGAGCTGGGGTAGCTAAATCAGAAGTGAGTCAACGTGTGTTTCTGCGCAAGTACCC  
-----+-----+-----+-----+-----+-----+ 1800  
a ACACCTCGACCCCATCGATTAGTCTTCACTCAGTTGCACACAAAGGACGCGTTCATGGG  
C G A G V A K S E V S Q R V F P A Q V P -

1801 GCACATGAAGCTGGTCTTGAGGCATCTAGTGGCGCGGTGCTGGAGCCATTGCAAGTTTCT  
-----+-----+-----+-----+-----+-----+ 1860  
a CGTGTACTTCGACCAGAAGTCCGTAGATCACCAGCGCCAGCACCTCGGTAACGTTCAAAGA  
A H E A G L E A S S G A V V E P L Q V S -

1861 GTGCCAGTAGCCGTAGAGAAAAGTGTCTTATCTGTTCGAGAAGGCGCGTGAGCTAAAGGCG  
-----+-----+-----+-----+-----+-----+ 1920  
a CACGGTCATCGGCATCTCTTTTGACAAAATAGACAGCTCTTCCGCGCACTCGATTTCGCG  
V P V A V E K T V L S V E K A R E L K A -

1921 GTAGATAAGGGCAAGGCGGTGCTGCACGCAAAGGAAGTCAAGAATGTACCGGTTAAGACG  
-----+-----+-----+-----+-----+-----+ 1980  
a CATCTATTCGCGTTCGCGCCAGCACGTGCGTTTCCTTCAAGTCTTACATGGCCAATTCGCG  
V D K G K A V V H A K E V K N V P V K T -

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**FIG. 18D**

```
1981 TTACCACGAGGGGCTCTAAAAATTAGTGAGGATACCGTTCGTAAGGAATTGTGCATGTTT
-----+-----+-----+-----+-----+-----+ 2040
a AATGGTGCTCCCGAGATTTTAACTACTCCTATGGCAAGCATTCTTAACACGTACAAA
L P R G A L K I S E D T V R K E L C M F -

2041 AGAACGTGTTCTGCGGCGTGACGTTGGACGTGTACAATGAAGCGACCATCGCCACTAGG
-----+-----+-----+-----+-----+ 2100
a TCTTGACAAGGACGCCGCACGTCAACCTGCACATGTTACTTCGCTGGTAGCGGTGATCC
R T C S C G V Q L D V Y N E A T I A T R -

2101 TTCTCAAATGCGTTTACCTTTGTGCGATAGCTTGAAAGGGAGGAGTGCGGTCTTTTTCTCA
-----+-----+-----+-----+-----+ 2160
a AAGAGTTTACGCAAATGGAAACAGCTATCGAACTTTCCCTCCTCACGCCAGAAAAAGAGT
F S N A F T F V D S L K G R S A V F F S -

2161 AAGCTGGGTGAGGGGTATACCTATAATGGTGGTAGCCATGTTTCATCAGGGTGGCCTCGT
-----+-----+-----+-----+-----+ 2220
a TTCGACCCACTCCCATATGGATATTACCACCATCGGTACAAAGTAGTCCCACCGGAGCA
K L G E G Y T Y N G G S H V S S G W P R -

2221 GCCCTAGAGGATATCTTAACGGCAATTAAGTACCCAAGCGTCTTCGACCACTGTTTAGTG
-----+-----+-----+-----+-----+ 2280
a CGGGATCTCCTATAGAATTGCCGTTAATTCATGGGTTCGAGAAGCTGGTGACAAATCAC
A L E D I L T A I K Y P S V F D H C L V -

2281 CAGAAGTACAAGATGGGTGGAGGCGTACCATTCCACGCTGATGACGAGGAGTGCTATCCA
-----+-----+-----+-----+-----+ 2340
a GTCTTCATGTTCTACCCACCTCCGCATGGTAAGGTGCGACTACTGCTCCTCACGATAGGT
Q K Y K M G G G V P F H A D D E E C Y P -

2341 TCAGATAACCCTATCTTGACGGTCAATCTCGTGGGGAAGGCAAACCTTCTCGACTAAGTGC
-----+-----+-----+-----+-----+ 2400
a AGTCTATTGGGATAGAAGTGCAGTTAGAGCACCCCTTCCGTTTGAAGAGCTGATTCACG
S D N P I L T V N L V G K A N F S T K C -

2401 AGGAAGGGTGGTAAGGTCATGGTCATAAACGTAGCTTCGGGTGACTATTTTCTTATGCCT
-----+-----+-----+-----+-----+ 2460
a TCCTTCCCACCATTCAGTACCAGTATTTGCATCGAAGCCCACTGATAAAAGAATACGGA
R K G G K V M V I N V A S G D Y F L M P -

2461 TGCGGTTTTCAAAGGACGCACTTGCATTAGTAAACTCCATCGACGAAGGGCGCATCAGT
-----+-----+-----+-----+-----+ 2520
a ACGCCAAAAGTTTCTGCGTGAACGTAAGTCATTTGAGGTAGCTGCTTCCCGCGTAGTCA
C G F Q R T H L H S V N S I D E G R I S -

2521 TTGACGTTTCAGGGCAACTCGGCGCGTCTTTGGTGTAGGCAGGATGTTGCAGTTAGCCGGC
-----+-----+-----+-----+-----+ 2580
a AACTGCAAGTCCCGTTGAGCCGCGCAGAAACCACATCCGTCCTACAACGTCAATCGGCCG
L T F R A T R R V F G V G R M L Q L A G -

2581 GGCGTGTGCGATGAGAAGTCACCAGGTGTTCCAAACCAGCAACCACAGAGCCAAGGTGCT
-----+-----+-----+-----+-----+ 2640
a CCGCACAGCCTACTCTTCAAGTGGTCCACAAGGTTTGGTGGTGTCTCGGTTCCACGA
G V S D E K S P G V P N Q Q P Q S Q G A -
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**FIG. 18E**

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2641 ACCAGAACAATCACACCAAAATCGGGGGGCAAGGCTCTATCTGAGGGAAGTGGTAGGGAA
-----+-----+-----+-----+-----+-----+ 2700
a TGGTCTTGTTAGTGTGGTTTTAGCCCCCGTTCCGAGATAGACTCCCTTCACCATCCCTT
T R T I T P K S G G K A L S E G S G R E -

2701 GTCAAGGGGAGGTCGACATACTCGATATGGTGCGAACAAGATTACGTTAGGAAGTGTGAG
-----+-----+-----+-----+-----+ 2760
a CAGTTCCCCTCCAGCTGTATGAGCTATAACCACGCTTGTTCATGAATCCTTCACACTC
V K G R S T Y S I W C E Q D Y V R K C E -

2761 TGGCTCAGGGCTGATAATCCAGTGATGGCTCTTRAACCTGGCTACACCCCAATGACATTT
-----+-----+-----+-----+-----+ 2820
a ACCGAGTCCCGACTATTAGGTCACCTACCGAGAAAYTTGGACCGATGTGGGGTTACTGTAAA
W L R A D N P V M A L ? P G Y T P M T F -

2821 GAAGTGGTTAAAGCCGGGACCTCTGAAGATGCCGTCGTGGAGTACTTGAAGTATCTGGCT
-----+-----+-----+-----+-----+ 2880
a CTTACCAATTTTCGGCCCTGGAGACTTCTACGGCAGCACCTCATGAAGTTATAGACCGA
E V V K A G T S E D A V V E Y L K Y L A -

2881 ATAGGCATTGGGAGGACATACAGGGCGTTGCTTATGGCTAGAAATATTGCCGTCCTACC
-----+-----+-----+-----+-----+ 2940
a TATCCGTAACCCTCCTGTATGTCCCGCAACGAATACCGATCTTTATAACGGCAGTGATGG
I G I G R T Y R A L L M A R N I A V T T -

2941 GCCGAAGGTGTTCTGAAAGTACCTAATCAAGTTTATGAATCACTACCGGGCTTTCACGTT
-----+-----+-----+-----+-----+ 3000
a CGGCTTCCACAAGACTTTCATGGATTAGTTCAAATACTTAGTGATGGCCCCGAAAGTGCAA
A E G V L K V P N Q V Y E S L P G F H V -

3001 TACAAGTCGGGCACAGATCTCATTTTTTCATTCAACACAAGACGGCTTGCGTGTGAGAGAC
-----+-----+-----+-----+-----+ 3060
a ATGTTACAGCCCGTGTCTAGAGTAAAAAGTAAGTTGTGTTCTGCCGAACGCACACTCTCTG
Y K S G T D L I F H S T Q D G L R V R D -

3061 CTACCGTACGTATTCATAGCTGAGAAAGGTATTTTTATCAAGGGCAAAGATGTCGACGCG
-----+-----+-----+-----+-----+ 3120
a GATGGCATGCATAAGTATCGACTCTTTCCATAAAAAATAGTTCCCGTTTCTACAGCTGCGC
L P Y V F I A E K G I F I K G K D V D A -

3121 GTAGTAGCTTTGGGCGACAATCTGTCCGTATGTGATGATATATTGGTTTTCCATGATGCT
-----+-----+-----+-----+-----+ 3180
a CATCATCGAAACCCGCTGTTAGACAGGCATACACTACTATATAACCAAAGGTACTACGA
V V A L G D N L S V C D D I L V F H D A -

3181 ATTAATTTGATGGGTGCACTGAAAGTTGCTCGATGTGGTATGGTGGGTGAATCATTTAAG
-----+-----+-----+-----+-----+ 3240
a TAATTAACTACCCACGTGACTTTCAACGAGCTACACCATACCACCCACTTAGTAAATTC
I N L M G A L K V A R C G M V G E S F K -

3241 TCGTTCGAATACAAATGCTATAATGCTCCCCCAGGTGGCGGTAAGACGACGATGCTAGTG
-----+-----+-----+-----+-----+ 3300
a AGCAAGCTTATGTTTACGATATTACGAGGGGGTCCACCGCCATTCTGCTGCTACGATCAC
S F E Y K C Y N A P P G G G K T T M L V -
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FIG. 18F

3301 GACGAATTTGTCAAGTCACCCAATAGCACGGCCACCATTACGGCTAACGTGGGAAGTTCT  
-----+-----+-----+-----+-----+-----+ 3360  
CTGCTTAAACAGTTCAGTGGGTTATCGTGCCGGTGGTAATGCCGATTGCACCCTTCAAGA  
a D E F V K S P N S T A T I T A N V G S S -

3361 GAGGACATAAATATGGCGGTGAAGAAGAGAGATCCGAATTTGGAAGGTCTCAACAGTGCT  
-----+-----+-----+-----+-----+-----+ 3420  
CTCCTGTATTTATACCGCCACTTCTTCTCTCTAGGCTTAAACCTTCCAGAGTTGTCACGA  
a E D I N M A V K K R D P N L E G L N S A -

3421 ACCACAGTTAACTCCAGGGTGGTTAACTTTATTGTCAGGGGAATGTATAAAAGGGTTTTG  
-----+-----+-----+-----+-----+-----+ 3480  
TGGTGTCAATTGAGGTCCCACCAATTGAAATAACAGTCCCCTTACATATTTTCCCAAAC  
a T T V N S R V V N F I V R G M Y K R V L -

3481 GTGGATGAGGTGTACATGATGCATCAAGGCTTACTACAACCTAGGCGTCTTCGCAACCGGC  
-----+-----+-----+-----+-----+-----+ 3540  
CACCTACTCCACATGTACTACGTAGTTCCGAATGATGTTGATCCGCAGAAGCGTTGGCCG  
a V D E V Y M M H Q G L L Q L G V F A T G -

3541 GCGTCGGAAGGCCTCTTTTTTGGAGACATAAATCAGATACCATTTCATAAACMGGGAGAAG  
-----+-----+-----+-----+-----+-----+ 3600  
CGCAGCCTTCCGGAGAAAAACCTCTGTATTTAGTCTATGGTAAGTATTTGKCCCTCTTC  
a A S E G L F F G D I N Q I P F I N R E K -

3601 GTGTTTAGGATGGATTGTGCTGTATTTGTTCCAAAGAAGGAAAGCGTTGTATACACTTCT  
-----+-----+-----+-----+-----+-----+ 3660  
CACAAATCCTACCTAACACGACATAAAACAAGGTTTCTTCCTTTCGCAACATATGTGAAGA  
a V F R M D C A V F V P K K E S V V Y T S -

3661 AAATCATACAGGTGTCCGTTAGATGTTTGCTACTTGTGTCTCAATGACCGTAAGGGGA  
-----+-----+-----+-----+-----+-----+ 3720  
TTTAGTATGTCCACAGGCAATCTACAAACGATGAACAACAGGAGTTACTGGCATTCCCCT  
a K S Y R C P L D V C Y L L S S M T V R G -

3721 ACGGAAAAGTGTTACCCTGAAAAGGTCGTTAGCGGTAAGGACAAACCAGTAGTAAGATCG  
-----+-----+-----+-----+-----+-----+ 3780  
TGCCTTTTCAATGGGACTTTTCCAGCAATCGCCATTCTGTTTGGTCATCATTCTAGC  
a T E K C Y P E K V V S G K D K P V V R S -

3781 CTGTCCAAAAGGCCAATTGGAACCACTGATGACGTAGCTGAAATAAACGCTGACGTGTAC  
-----+-----+-----+-----+-----+-----+ 3840  
GACAGGTTTTCCGGTTAACCTTGGTGACTACTGCATCGACTTTATTTGCGACTGCACATG  
a L S K R P I G T T D D V A E I N A D V Y -

3841 TTGTGCATGACCCAGTTGGAGAAGTCGGATATGAAGAGGTGCTTGAAGGGAAAAGGAAAA  
-----+-----+-----+-----+-----+-----+ 3900  
AACACGTACTGGGTCAACCTCTTCAGCCTATACTTCTCCAGCAACTTCCCTTTTCTTTTT  
a L C M T Q L E K S D M K R S L K G K G K -

3901 GAAACACCAGTGATGACAGTGCATGAAGCACAGGGAAAACATTTCAGTGATGTGGTATTG  
-----+-----+-----+-----+-----+-----+ 3960  
CTTTGTGGTCACTACTGTACGTACTTCGTGTCCCTTTTTGTAAGTCACTACACCATAAC  
a E T P V M T V H E A Q G K T F S D V V L -



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FIG. 18G

3961 TTTAGGACGAAGAAAGCCGATGACTCCCTATTCTACTAAACAACCGCATATACTTGTGGT 4020  
-----+-----+-----+-----+-----+-----+  
a AAATCCTGCTTCTTTTCGGCTACTGAGGGATAAGTGATTGTGGCGTATATGAACAACCA  
F R T K K A D D S L F T K Q P H I L V G -  
  
4021 TTGTTCGAGACACACACGCTCACTGGTTTATGCCGCTCTGAGCTCAGAGTTGGACGATAAG 4080  
-----+-----+-----+-----+-----+-----+  
a AACAGCTCTGTGTGTGCGAGTGACCAAATACGGCGAGACTCGAGTCTCAACCTGCTATTTC  
L S R H T R S L V Y A A L S S E L D D K -  
\* A Q S W T I R -  
  
(FRAMESHIFT)  
4081 GTCGGCACATATATTAGCGACGCGTCGCTCAATCAGTATCCGACGCTTTGCTTCACACG 4140  
-----+-----+-----+-----+-----+-----+  
a CAGCCGTGTATATAATCGCTGCGCAGCGGAGTTAGTCATAGGCTGCCAAACGAAGTGTGC  
V G T Y I S D A S P Q S V S D A L L H T -  
S A H I L A T R H L N Q Y P T L C F T R -  
  
ORF1b (RdRp)  
4141 TTCGCCCCGGCTGGTTGCTTTTCGAGGTATATGAGCGTATGAATTTTGGACCGACCTTCGA 4200  
-----+-----+-----+-----+-----+-----+  
a AAGCGGGGCGCCACCAACGAAAGCTCCATATACTCGCATACTTAAACCTGGCTGGAAGCT  
F A P A G C F R G I \* -  
b S P R L V A F E V Y E R M N F G P T F E -  
  
4201 AGGGGAGTTGGTACGGAAGATACCAACAAGTCATTTTGTAGCCGTGAATGGGTTTCTCGA 4260  
-----+-----+-----+-----+-----+-----+  
b TCCCCTCAACCATGCCTTCTATGGTTGTTTCAGTAAACATCGGCACTTACCCAAAGAGCT  
G E L V R K I P T S H F V A V N G F L E -  
  
4261 GGACTTACTCGACGGTTGTCCGGCTTTTCGACTATGACTTCTTTGAGGATGATTTCGAAAC 4320  
-----+-----+-----+-----+-----+-----+  
b CCTGAATGAGCTGCCAACAGGCCGAAAGCTGATACTGAAGAACTCCTACTAAAGCTTTG  
D L L D G C P A F D Y D F F E D D F E T -  
  
4321 TTCAGATCAGTCTTTCTCTCATAGAAGATGTGCGCATTTCTGAATCTTTTTCTCATTTTGC 4380  
-----+-----+-----+-----+-----+-----+  
b AAGTCTAGTCAGAAAGGAGTATCTTCTACACGCGTAAAGACTTAGAAAAAGAGTAAACG  
S D Q S F L I E D V R I S E S F S H F A -  
  
4381 GTCGAAAATAGAGGATAGGTTTTACAGTTTTATTAGGTCTAGCGTAGGTTTACCAAAGCG 4440  
-----+-----+-----+-----+-----+-----+  
b CAGCTTTTATCTCCTATCCAAAATGTCAAATAATCCAGATCGCATCCAAATGGTTTCGC  
S K I E D R F Y S F I R S S V G L P K R -  
  
4441 CAACACCTTGAAGTGTAACCTCGTCACGTTTGAAAATAGGAATTCCAACGCCGATCGCGG 4500  
-----+-----+-----+-----+-----+-----+  
b GTTGTGGAACCTTCACATTGGAGCAGTGCAAACCTTTTATCCTTAAGGTTGCGGCTAGCGCC  
N T L K C N L V T F E N R N S N A D R G -  
  
4501 TTGTAACGTGGGTTGTGACGACTCTGTGGCGCATGAACTGAAGGAGATTTTCTTCGAGGA 4560  
-----+-----+-----+-----+-----+-----+  
b AACATTGCACCCAACACTGCTGAGACACCGCGTACTTGACTTCCTCTAAAAGAAGCTCCT  
C N V G C D D S V A H E L K E I F F E E -

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**FIG. 18H**

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4561  GGTCTTAACAAAGCTCGTTTAGCAGAGGTGACGGAAGCCATTTGTCCAGCAACACGAT
-----+-----+-----+-----+-----+-----+ 4620
CCAGCAATTGTTTCGAGCAAATCGTCTCCACTGCCTTTCGGTAAACAGGTCGTTGTGCTA
b    V V N K A R L A E V T E S H L S S N T M -

4621  GTTGTATATCAGATTGGTTGGACAAAAGGGCACCTAACGCTTACAAGTCTCTCAAGCGGGC
-----+-----+-----+-----+-----+-----+ 4680
CAACAATAGTCTAACCAACCTGTTTTCCCGTGGATTGCGAATGTTTCAGAGAGTTCGCCCG
b    L L S D W L D K R A P N A Y K S L K R A -

4681  TTTAGGTTTCGGTTGTCTTTTCATCCGCTCTATGTTGACGCTCTTATACGCTCATGGTGAAAGC
-----+-----+-----+-----+-----+-----+ 4740
AAATCCAAGCCAACAGAAAGTAGGCAGATACAACCTGCAGAATATGCGAGTACCACTTTTCG
b    L G S V V F H P S M L T S Y T L M V K A -

4741  AGACGTAAAACCCAAGTTGGACAATACGCCATTGTGCAAGTACGTAACGGGGCAGAATAT
-----+-----+-----+-----+-----+-----+ 4800
TCTGCATTTTGGGTTCAACCTGTTATGCGGTAACAGCTTCATGCATTGCCCGCTCTTATA
b    D V K P K L D N T P L S K Y V T G Q N I -

4801  AGTCTACCACGATAGGTGCGTAACTGCGCTTTTTTCTTGCAATTTTACTGCGTGCGTAGA
-----+-----+-----+-----+-----+-----+ 4860
TCAGATGGTGCCTATCCACGCATTGACGCGAAAAAAGAACGTAAAAATGACGCACGCATCT
b    V Y H D R C V T A L F S C I F T A C V E -

4861  GCGCTTAAAATACGTAGTGGACGAAAGGTGGCTCTTCTACCACGGGATGGACACTGCGGA
-----+-----+-----+-----+-----+-----+ 4920
CGCGAATTTTATGCATCACCTGCTTTCCACCGAGAAGATGGTGCCCTACCTGTGACGCCT
b    R L K Y V V D E R W L F Y H G M D T A E -

4921  GTTGGCGGCTGCATTGAGGAACAATTTGGGGGACATCCGGCAATACTACACCTATGAACT
-----+-----+-----+-----+-----+-----+ 4980
CAACCGCCGACGTAACCTCCTTGTTAAACCCCTGTAGGCCGTTATGATGTGGATACTTGA
b    L A A A L R N N L G D I R Q Y Y T Y E L -

4981  GGATATCAGTAAGTACGACAAATCTCAGAGTGCTCTCATGAAGCAGGTGGAGGAGTTGAT
-----+-----+-----+-----+-----+-----+ 5040
CCTATAGTCATTGCTGCTTTAGAGTCTCAGGAGTACTTCGTCCACCTCCTCAACTA
b    D I S K Y D K S Q S A L M K Q V E E L I -

5041  ACTCTTGACACTTGGTGTGATAGAGAAGTTTTGTCTACTTTCTTTTGTGGTGAGTATGA
-----+-----+-----+-----+-----+-----+ 5100
TGAGAACTGTGAACCACAACCTATCTCTTCAAACAGATGAAAGAAAACACCACTCATACT
b    L L T L G V D R E V L S T F F C G E Y D -

5101  TAGCGTCGTGAGAACGATGACGAAGGAATTGGTGTGTCTGTCGGCTCTCAGAGGCGCAG
-----+-----+-----+-----+-----+-----+ 5160
ATCGCAGCACTCTTGCTACTGCTTCCTTAACCACAACAGACAGCCGAGAGTCTCCGCGTC
b    S V V R T M T K E L V L S V G S Q R R S -

5161  TGGTGGTGCTAACACGTGGTTGGGAAATAGTTTAGTCTTGTGCACCTTGTGTCCGTAGT
-----+-----+-----+-----+-----+-----+ 5220
ACCACCACGATTGTGCACCAACCTTTTATCAAATCAGAACACGTGGAACAACAGGCATCA
b    G G A N T W L G N S L V L C T L L S V V -

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FIG. 18I

5221 ACTTAGGGGATTAGATTATAGTTATATTGTAGTTAGCGGTGATGATAGCCTTATATTTAG  
-----+-----+-----+-----+-----+-----+ 5280  
TGAATCCCCTAATCTAATATCAATATAACATCAATCGCCACTACTATCGGAATATAAATC  
b L R G L D Y S Y I V V S G D D S L I F S -

5281 TCGGCAGCCGTTGGATATTGATACGTCGGTCTGAGCGATAATTTTGGTTTTGACGTAAA  
-----+-----+-----+-----+-----+-----+ 5340  
AGCCGTCGGCAACCTATAACTATGCAGCCAAGACTCGCTATTAAAACCAAACTGCATTT  
b R Q P L D I D T S V L S D N F G F D V K -

5341 GATTTTAAACCAAGCTGCTCCATATTTTGTCTAAGTTTGTAGTTCAAGTCGAGGATAG  
-----+-----+-----+-----+-----+-----+ 5400  
CTAAAAATGGTTCGACGAGGTATAAAAACAAGATTCAAAAATCAAGTTCAGCTCCTATC  
b I F N Q A A P Y F C S K F L V Q V E D S -

5401 TCTCTTTTGTTCCTCCGATCCACTTAACTCTTCGTTAAGTTTGGAGCTTCCAAAACCTTC  
-----+-----+-----+-----+-----+-----+ 5460  
AGAGAAAAACAAGGGCTAGGTGAATTTGAGAAGCAATTCAAACCTCGAAGGTTTGAAG  
b L F F V P D P L K L F V K F G A S K T S -

5461 AGATATCGACCTTTTACATGAGATTTTCAATCTTTCGTCGATCTTTCGAAGGGTTTCAA  
-----+-----+-----+-----+-----+-----+ 5520  
TCTATAGCTGGAAAATGTACTCTAAAAAGTTAGAAAGCAGCTAGAAAGCTTCCCAAAGTT  
b D I D L L H E I F Q S F V D L S K G F N -

5521 TAGAGAGGACGTCATCCAGGAATTAGCTAAGCTGGTGACGCGGAAATATAAGCATTCTGGG  
-----+-----+-----+-----+-----+-----+ 5580  
ATCTCTCCTGCAGTAGGTCTTAATCGATTTCGACCACTGCGCCTTTATATTCTGTAAGCCC  
b R E D V I Q E L A K L V T R K Y K H S G -

5581 ATGGACCTACTCGGCTTTGTGTGTCTTGCACGTTTTAAGTGCAAATTTTTCGCAGTTCTG  
-----+-----+-----+-----+-----+-----+ 5640  
TACCTGGATGAGCCGAAACACACAGAACGTGCAAATTCACGTTTAAAAGCGTCAAGAC  
b W T Y S A L C V L H V L S A N F S Q F C -

5641 TAGGTTATATTACCACAATAGCGTGAATCTCGATGTGCGCCCTATTCAGAGGACCGAGTC  
-----+-----+-----+-----+-----+-----+ 5700  
ATCCAATATAATGGTGTATCGCACTTAGAGCTACACGCGGGATAAGTCTCCTGGCTCAG  
b R L Y Y H N S V N L D V R P I Q R T E S -

5701 GCTTTCCTTGCTGGCCTTGAAGGCAAGAATTTTAAGGTGAAAGCTTCTCGTTTTGCCTT  
-----+-----+-----+-----+-----+-----+ 5760  
CGAAAGGAACGACCGGAACCTTCCGTTCTTAAATTCACCTTTCGAAGAGCAAAACGGAA  
b L S L L A L K A R I L R W K A S R F A F -

5761 TTCGATAAAGAGGGGTTAATCGCGTTGGCCACGCTATAGTGTCTGTGCCTCGGTTCTT  
-----+-----+-----+-----+-----+-----+ 5820  
AAGCTATTTCTCCCAATTAGCGCAACCGGTGCGATATCACAAAGACACGGAGCCAAGAA  
b S I K R G \* -

5821 CGTGAGGTTAATACCGAAGGGTCGTCTACTTATCTCAGTTATTTATTTTTCTGCTTCT  
-----+-----+-----+-----+-----+-----+ 5880  
GCACTCCAATTATGGCTTCCCAGCAGCATGAATAGAGTCAATAAATAAAAAGCAGAAGA

5881 CTTAGGCGTGCCATCCGTGAAGTTAATACCGGTGGCACTCCTTCTCGAAGTGGGTATTAA  
-----+-----+-----+-----+-----+-----+ 5940  
GAATCCGCACGGTAGGCACTTCAATTATGGCCACCGTGAGGAAGAGCTTCAACCATAATT

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**FIG. 18J**

AGACCAAAATTTTTATTGTGTGTACTTTTTGTTTTGTTACACCCGTGAGGACAAGACC  
5941 -----+-----+-----+-----+-----+ 6000  
TCTGGTTTTAAAAATAAACACACATGAAAAACAAAACAAGTGTGGCACTCCTGTTCTGG

**ORF2 (7K)**

GGTGAACATGTACAGTAGAGGGTCTTTCTTTAAGTCTCGGGTTACCCTTCTACTCTTG  
6001 -----+-----+-----+-----+-----+ 6060  
CCACCTTGATACATGTCATCTCCAGAAAGAAATTCAGAGCCCAATGGGAAGGATGAGAAC  
c M Y S R G S F F K S R V T L P T L V -

TCGGAGCATAACATGTGGGAGTTTGAACCTCCGTATCTTACGGACAAGAGACACATCAGCT  
6061 -----+-----+-----+-----+-----+ 6120  
AGCCTCGTATGTACACCCTCAAACCTTGAGGGCATAGAATGCCTGTTCTCTGTGTAGTCTGA  
c G A Y M W E F E L P Y L T D K R H I S Y -

ATAGCGCGCCAAGTGTGCGGACTTTTAGCCTTGTGTGCGAGGTAGGATAGGGGCCAACAGG  
6121 -----+-----+-----+-----+-----+ 6180  
TATCGCGCGGTTTACAGCGCTGAAATCGGAACACAGCTCCATCCTATCCCCGGTTGTCC  
c S A P S V A T F S L V S R \* -

TGACCAACAGCCTGCACTTAAGGTGCGCTGGAAGTGTGGATTGTTGCTCAGTGTGCCAA  
6181 -----+-----+-----+-----+-----+ 6240  
ACTGGTTGTGCGACGTGAATTCCACGCGACCTTCACAACCTAAACCAGAGTCACACGGTT

ATATCCTTTTAGGCGATGTACAGGAGTCTAGTTTAGTGTGTCTTTGGGGGATGACGGGAG  
6241 -----+-----+-----+-----+-----+ 6300  
TATAGGAAAATCCGCTACATGTCTCAGATCAAATCACACAGAAACCCCTACTGCCCTC

CGACTAGGTTTAGGACTGTAGCTGCTATGTAAGTCGTGCATGCGGCATTGTGCGTAAGAC  
6301 -----+-----+-----+-----+-----+ 6360  
GCTGATCCAAATCCTGACATCGACGATACATTACGACGTACGCCGTAACACGCATTCTG

GTGCATGCATTTGGGCGAGTGCCCTAGGGCAGCGTCGGTCAGGTGACTAGCAGCCGGGCTC  
6361 -----+-----+-----+-----+-----+ 6420  
CACGTACGTAAACCCGCTCACGGGATCCCGTCGCAGCCAGTCCACTGATCGTCGGCCGAG

TACGGAGCGCTGAAAGTGCTAGGTCCTGAAGGTACAGTTGGGCTGAGGCAGGACATGGTT  
6421 -----+-----+-----+-----+-----+ 6480  
ATGCCTCGCGACTTTCAGATCCAGGACTTCCATGTCAACCCGACTCCGTCTGTACCAA

GAACGAGTTGACCGTGGGGACCAGCGGCGGTGACTCGGGCCGTAGCCACGCGCGGGCGG  
6481 -----+-----+-----+-----+-----+ 6540  
CTTGCTCAACTGGCACCCCTGGTCGCCGCCACTGAGCCCGCATCGGTGCGCGCCCCGCC

CAGGGCGTCTCGTGGTGTATCTGGGCAAGATACGGCTTTATTAGGCACCATAATATGGAG  
6541 -----+-----+-----+-----+-----+ 6600  
GTCCCGCAGAGCACCACATAGACCGTTCTATGCCGAAATAATCCGTGGTATTATACCTC

CCCAAAGCGTCGGGGTCGGGAAACATCTCCATAGCTTAGTGGCAGCAGCCTAAGATAGGC  
6601 -----+-----+-----+-----+-----+ 6660  
GGGTTTCGCAGCCCCAGCCCTTTGTAGAGGTATCGAATCACCGTCGTCCGATTCTATCCG

TGGGAGGCCCGTTCCCTGTAGTAGTGGTGGGTTAGCATGCCACTAAGCGGTGCGGCGTGA  
6661 -----+-----+-----+-----+-----+ 6720  
ACCCTCCGGGCAAGGGACATCATCACCAACCAATCGTACGGTGATTCGCCACGCCGCACT

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**FIG. 18K**

TAAGGCGCCACCGTCCGTAGTTAGGCGACCCGTGTTTTAATAGGGTCTCTTTAGTTAAAGT  
6721 -----+-----+-----+-----+-----+-----+ 6780  
ATTCCGCGGTGGCAGGCATCAATCCGCTGGGCACAAAATTATCCAGAGAAATCAATTCA  
  
TTAGGCATGTCGTACAGTTAGGATTTCTTTTTAGATATTCTTTTATTTTTTATTGTTTGT  
6781 -----+-----+-----+-----+-----+-----+ 6840  
AATCCGTACAGCATGTCAATCCTAAAGAAAAATCTATAAGAAAAATAAAAAATAACAAACA  
  
TAGTTTAGATGTACATTATTACGTAGGTTACTTTGGCGCTACGCCAGAGGTTTTTCCTCT  
6841 -----+-----+-----+-----+-----+-----+ 6900  
ATCAAATCTACATGTAATAATGCATCCAATGAAACCGCGATGCGGTCTCCAAAAGGAGA  
  
TTGTGTGTAGCCTTTAATGTAGGTTTCTTTGTTTTATTTTTGCCTTTCAGGCGGCGCGTT  
6901 -----+-----+-----+-----+-----+-----+ 6960  
AACACACATCGGAAATTACATCCAAAGAAACAAAATAAAAACGGAAAGTCCGCCGCGCAA  
  
TCTTTTCTTCTATTTAGGTTTATCTTCTTTCTTTAGTGTGTGTCGTATATGACGCTACGTC  
6961 -----+-----+-----+-----+-----+-----+ 7020  
AGAAAAGAAGATAAATCCAAATAGAAGAAAGGAATCACACAGCATATACTGCGATGCAG  
  
CAAATTATGAATTTTCTTTCGTGTAGGCGTCGTTGAGTGCCTTCATCGGCGCTAGACGAG  
7021 -----+-----+-----+-----+-----+-----+ 7080  
GTTTAATACTTAAAAGGAAGCACATCCGCAGCAACTCACGCAAGTAGCCGCGATCTGCTC  
  
GTTTAGTGGCGACATAAATAGGTTTTTGCGCGAGATTGGGATAGAACGAGTTTCGCCTTAA  
7081 -----+-----+-----+-----+-----+-----+ 7140  
CAAATCACCGCTGTATTTATCCAAAACGCGCTCTAACCCTATCTTGCTCAAGCGGAATT  
  
AAGAGAAATCGGGGAAGGCGCCACGCGAATGACCTTCGTGCTGAGCGAAGGTAGTATCGT  
7141 -----+-----+-----+-----+-----+-----+ 7200  
TTCTCTTTAGCCCCCTCCGCGGTGCGCTTACTGGAAGCACGACTCGCTTCCATCATAGCA

**ORF3 (5K, Membrane protein)**

GATTTTATATTGAAGTAGGCGTATTTGTTTTATGGATGATTTTAAACAGGCAATACTGTTG  
7201 -----+-----+-----+-----+-----+-----+ 7260  
CTAAAATATAACTTCATCCGCATAAAACAAATACCTACTAAAATTTGTCCGTTATGACAAC  
a M D D F K Q A I L L -

CTAGTAGTCGATTTTGTCTTCGTGATAATTCTGCTGCTGGTTCTTACGTTTCGTGCTCCCG  
7261 -----+-----+-----+-----+-----+-----+ 7320  
GATCATCAGCTAAAACAGAAGCACTATTAAGACGACGACCAAGAATGCAAGCAGCAGGGC  
a L V V D F V F V I I L L L V L T F V V P -

AGGTTACAGCAAAGCTCCACCATTAAATACAGGTCTTAGGACAGTGTGATTCTCCTTTAG  
7321 -----+-----+-----+-----+-----+-----+ 7380  
TCCAATGTCGTTTCGAGGTGGTAATTATGTCCAGAATCCTGTACACTAAGGAGGAAATC  
a R L Q Q S S T I N T G L R T V \* -

**ORF4 (HSP70 Homolog)**

TTAGATATGGAAGTAGGTATAGATTTTGAACCACTTTCAGCACAATCTGCTTTTCCCCA  
7381 -----+-----+-----+-----+-----+-----+ 7440  
AATCTATACCTTCATCCATATCTAAAACCTTGGTGAAAGTCGTGTTAGACGAAAAGGGGT  
a M E V G I D F G T T F S T I C F S P -

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FIG. 18L

7441 TCTGGGGTCACGGTTGTACTCCTGTGGCCGGTAGTGTTTACGTTGAAACCCAAATTTTTT  
+-----+-----+-----+-----+-----+-----+ 7500  
AGACCCAGTCGCCAACATGAGGACACCGCCATCACAAATGCAACTTTGGGTTTAAAAA  
a S G V S G C T P V A G S V Y V E T Q I F -

7501 ATACCTGAAGGTAGCAGTACTTACTTAATTGGTAAAGCTGCGGGGAAAGCTTATCGTGAC  
+-----+-----+-----+-----+-----+-----+ 7560  
TATGGACTTCCATCGTCATGAATGAATTAACCATTTTCGACGCCCTTTTGAATAGCACTG  
a I P E G S S T Y L I G K A A G K A Y R D -

7561 GGTGTAGAGGGAAGGTTGTATGTTAACCCGAAAAGGTGGGCAGGTGTGACGAGGGATAAC  
+-----+-----+-----+-----+-----+-----+ 7620  
CCACATCTCCCTTCCAACATACAATTGGGCTTTTCCACCCGTCCACACTGCTCCCTATTG  
a G V E G R L Y V N P K R W A G V T R D N -

7621 GTCGAACGCTACGTCGAGAAATTAAACCTACATACACCGTGAAGATAGACAGCGGAGGC  
+-----+-----+-----+-----+-----+-----+ 7680  
CAGCTTGCATGACGCTCTTTAATTTTGGATGTATGTGGCACTTCTATCTGTGCCTCCG  
a V E R Y V E K L K P T Y T V K I D S G G -

7681 GCCTTATTAATTGGAGGTTTAGGTTCCGGACCAGACACCTTATTGAGGGTCGTTGACGTA  
+-----+-----+-----+-----+-----+-----+ 7740  
CGGAATAATTAACCTCCAAATCCAAGGCCTGGTCTGTGGAATAACTCCCAGCAACTGCAT  
a A L L I G G L G S G P D T L L R V V D V -

7741 ATATGTTTATTCTTGAGAGCCTTGATACTGGAGTCCGAAAGGTATACGTCTACGACGGTT  
+-----+-----+-----+-----+-----+-----+ 7800  
TATACAAATAAGAACTCTCGGAATATGACCTCACGCTTTCCATATGCAGATGCTGCCAA  
a I C L F L R A L I L E C E R Y T S T T V -

7801 ACAGCAGCTGTTGTAACGGTACCGGCTGACTATAACTCCTTTAAACGAAGCTTCGTTGTT  
+-----+-----+-----+-----+-----+-----+ 7860  
TGTCGTCGACAACATTGCCATGGCCGACTGATATTGAGGAAATTTGCTTCGAAGCAACAA  
a T A A V V T V P A D Y N S F K R S F V V -

7861 GAGGCGCTAAAAGGTCTTGGTATACCGGTTAGAGGTGTTGTTAACGAACCGACGGCCGCA  
+-----+-----+-----+-----+-----+-----+ 7920  
CTCCGCGATTTTCCAGAACCATATGGCCAATCTCCACAACAATTGCTTGGCTGCCGGCGT  
a E A L K G L G I P V R G V V N E P T A A -

7921 GCCCTCTATTCCTTAGCTAAGTCGCGAGTAGAAGACCTATTATTAGCGGTTTTTGATTTT  
+-----+-----+-----+-----+-----+-----+ 7980  
CGGGAGATAAGGAATCGATTGACGCTCATCTTCTGGATAATAATCGCCAAAAACTAAAA  
a A L Y S L A K S R V E D L L L A V F D F -

7981 GGGGGAGGGACTTTTCGACGTCTCATTCGTTAAGAAGAAGGGAAATATACTATGCGTCATC  
+-----+-----+-----+-----+-----+-----+ 8040  
CCCCCTCCCTGAAAGCTGCAGAGTAAGCAATTCTTCTCCCTTTATATGATACGCAGTAG  
a G G G T F D V S F V K K K G N I L C V I -

8041 TTTTCAGTGGGTGATAATTTCTTGGGTGGTAGAGATATTGATAGAGCTATCGTGGAAGTT  
+-----+-----+-----+-----+-----+-----+ 8100  
AAAAGTCACCCACTATTAAAGAACCACCATCTCTATAACTATCTCGATAGCACCTTCAA  
a F S V G D N F L G G R D I D R A I V E V -

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FIG. 18M

8101 ATCAAACAAAAGATCAAAGGAAAGGCGTCTGATGCCAAGTTAGGGATATTCGTATCCTCG  
-----+-----+-----+-----+-----+ 8160  
TAGTTTGTTCCTTTCTAGTTTCCTTTCCGCAGACTACGGTTCAATCCCTATAAGCATAGGAGC  
a I K Q K I K G K A S D A K L G I F V S S -

8161 ATGAAGGAAGACTTGTCTAACAATAACGCTATAACGCAACACCTTATCCCCGTAGAAGGG  
-----+-----+-----+-----+ 8220  
TACTTCCTTCTGAACAGATTGTTATTGCGATATTGCGTTGTGGAATAGGGGCATCTTCCC  
a M K E D L S N N N A I T Q H L I P V E G -

8221 GGTGTGGAGGTTGTGGATTTGACTAGCGACGAACTGGACGCAATCGTTGCACCATTCAGC  
-----+-----+-----+-----+ 8280  
CCACACCTCCAACACCTAAACTGATCGCTGCTTGACCTGCGTTAGCAACGTGGTAAGTCG  
a G V E V V D L T S D E L D A I V A P F S -

8281 GCTAGGGCTGTGGAAGTATTCAAACTGGTCTTGACAACCTTTTACCCAGACCCGGTTATT  
-----+-----+-----+-----+ 8340  
CGATCCCAGACCTTCATAAGTTTGTGACCAGAACTGTTGAAAATGGGTCTGGGCCAATAA  
a A R A V E V F K T G L D N F Y P D P V I -

8341 GCCGTTATGACTGGGGGGTCAAGTGCTCTAGTTAAGGTCAGGAGTGATGTGGCTAATTTG  
-----+-----+-----+-----+ 8400  
CGGCAATACTGACCCCCAGTTTCACGAGATCAATTCAGTCCTCACTACACCGATTAAAC  
a A V M T G G S S A L V K V R S D V A N L -

8401 CCGCAGATATCTAAAGTCGTGTTTCGACAGTACCGATTTTAGATGTTCCGTGGCTTGTGGG  
-----+-----+-----+-----+ 8460  
GGCGTCTATAGATTTTCAGCACAAGCTGTCTATGGCTAAAATCTACAAGCCACCGAACCCC  
a P Q I S K V V F D S T D F R C S V A C G -

8461 GCTAAGGTTTACTGCGATACTTTGGCAGGTAATAGCGGACTGAGACTGGTGGACACTTTA  
-----+-----+-----+-----+ 8520  
CGATTCCAAATGACGCTATGAAACCGTCCATTATCGCCTGACTCTGACCACCTGTGAAAT  
a A K V Y C D T L A G N S G L R L V D T L -

8521 ACGAATACGCTAACGGACGAGGTAGTGGGTCTTCAGCCGGTGGTAATTTTCCCGAAAGGT  
-----+-----+-----+-----+ 8580  
TGCTTATGCGATTGCCTGCTCCATCACCAGAACTCGGCCACCATTAAGGGCTTTCCA  
a T N T L T D E V V G L Q P V V I F P K G -

8581 AGTCCAATACCCTGTTTCATATACTCATAGATACACAGTGGGTGGTGGAGATGTGGTATAC  
-----+-----+-----+-----+ 8640  
TCAGGTTATGGGACAAGTATATGAGTATCTATGTGTACCCACCACCTCTACACCATATG  
a S P I P C S Y T H R Y T V G G G D V V Y -

8641 GGTATATTTGAAGGGGAGAATAACAGAGCTTTTCTAAATGAGCCGACGTTCCGGGGCGTA  
-----+-----+-----+-----+ 8700  
CCATATAAACTTCCCCTCTTATTGTCTCGAAAAGATTTACTCGGCTGCAAGGCCCCGCAT  
a G I F E G E N N R A F L N E P T F R G V -

8701 TCGAAACGTAGGGGAGACCCAGTAGAGACCGACGTGGCGCAGTTTAATCTCTCCACGGAC  
-----+-----+-----+-----+ 8760  
AGCTTTGCATCCCCCTCTGGGTCTCTGGCTGCACCGCGTCAAATTAGAGAGGTGCCTG  
a S K R R G D P V E T D V A Q F N L S T D -

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**FIG. 18N**

8761 GGAACGGTGTCTGTTATCGTTAATGGTGAGGAAGTAAAGAATGAATATCTGGTACCCGGG + 8820  
-----+-----+-----+-----+-----+  
a CCTTGCCACAGACAATAGCAATTACCACTCCTTCATTTCTTACTTATAGACCATGGGCCC  
G T V S V I V N G E E V K N E Y L V P G -

8821 ACAACAAACGTACTGGATTTCATTGGTCTATAAATCTGGGAGAGAAGATTTAGAGGCTAAG + 8880  
-----+-----+-----+-----+-----+  
a TGTGTTTGCATGACCTAAGTAACCAGATATTTAGACCCTCTCTTCTAAATCTCCGATTCT  
T T N V L D S L V Y K S G R E D L E A K -

8881 GCAATACCAGAGTACTTGACCACACTGAATATTTTGCACGATAAGGCTTTTCACGAGGAGA + 8940  
-----+-----+-----+-----+-----+  
a CGTTATGGTCTCATGAACTGGTGTGACTTATAAAACGTGCTATTCCGAAAGTGCTCCTCT  
A I P E Y L T T L N I L H D K A F T R R -

8941 AACCTGGGTAACAAAGATAAGGGGTTCTCGGATTTAAGGATAGAAGAAAATTTTAAATAA + 9000  
-----+-----+-----+-----+-----+  
a TTGGACCCATTGTTTCTATTCCCAAGAGCCTAAATTCCTATCTTCTTTTAAAAAATTTT  
N L G N K D K G F S D L R I E E N F L K -

**ORF5 (HSP90 Homolog)**

9001 TCCGCCGTAGATACAGACACGATTTTGAATGGATAAATATATTTATGTAACGGGGATATT + 9060  
-----+-----+-----+-----+-----+  
a AGGCGGCATCTATGTCTGTGCTAAACTTACCTATTTATATAAATACATTGCCCTATAA  
S A V D T D T I L N G \*  
b M D K Y I Y V T G I L -

9061 AAACCCTAACGAGGCTAGAGACGAGGTATTCTCGGTAGTGAATAAGGGATATATTGGACC + 9120  
-----+-----+-----+-----+-----+  
b TTTGGGATTGCTCCGATCTCTGCTCCATAAGAGCCATCACTTATCCCTATATAACCTGG  
N P N E A R D E V F S V V N K G Y I G P -

9121 GGGAGGGCGCTCCTTTTTCGAATCGTGGTAGTAAGTACACCGTCGTCTGGGAAACTCTGC + 9180  
-----+-----+-----+-----+-----+  
b CCCTCCCGCGAGGAAAAGCTTAGCACCATCATTCATGTGGCAGCAGACCCTTTTGAGACG  
G G R S F S N R G S K Y T V V W E N S A -

9181 TGCGAGGATTAGTGGATTTACGTCGACTTCGCAATCTACGATAGATGCTTTTCGCGTATTT + 9240  
-----+-----+-----+-----+-----+  
b ACGCTCCTAATCACCTAAATGCAGCTGAAGCGTTAGATGCTATCTACGAAAGCGCATAAA  
A R I S G F T S T S Q S T I D A F A Y F -

9241 CTTGTTGAAAGGCGGATTGACTACCACGCTCTCTAACCCAATAAACTGTGAGAATTGGGT + 9300  
-----+-----+-----+-----+-----+  
b GAACAACCTTCCGCCTAACTGATGGTGCAGAGATTGGGTATTTGACACTCTTAACCCA  
L L K G G L T T T L S N P I N C E N W V -

9301 CAGGTCATCTAAGGATTTAAGCGCGTTTTTTCAGGACCCTAATTAAAGGTAAGATTTATGC + 9360  
-----+-----+-----+-----+-----+  
b GTCCAGTAGATTCTAAATTCGCGCAAAAAGTCCTGGGATTAATTTCCATTCTAAATACG  
R S S K D L S A F F R T L I K G K I Y A -

9361 ATCGCGTTCTGTGGACAGCAATCTTCCAAAGAAAGACAGGGATGACATCATGGAAGCGAG + 9420  
-----+-----+-----+-----+-----+  
b TAGCGCAAGACACCTGTCGTTAGAAGGTTTCTTTCTGTCCCTACTGTAGTACCTTCGCTC  
S R S V D S N L P K K D R D D I M E A S -



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FIG. 180

TCGACGACTATCGCCATCGGACGCCGCCCTTTTGCAGAGCAGTGTGCGTTTCAGGTAGGGAA  
9421 -----+-----+-----+-----+-----+-----+ 9480  
AGCTGCTGATAGCGGTAGCCTGCGGCGGAAAACGTCTCGTCACAGCCAAGTCCATCCCTT  
b R R L S P S D A A F C R A V S V Q V G K -

GTATGTGGACGTAACGCAGAATTTAGAAAGTACGATCGTGCCGTTAAGAGTTATGGAAAT  
9481 -----+-----+-----+-----+-----+-----+ 9540  
CATACACCTGCATTGCGTCTTAAATCTTTTCATGCTAGCACGGCAATTCTCAATACCTTTA  
b Y V D V T Q N L E S T I V P L R V M E I -

AAAGAAAAGACGAGGATCAGCACATGTTAGTTTACCGAAGGTGGTATCCGCTTACGTAGA  
9541 -----+-----+-----+-----+-----+-----+ 9600  
TTTCTTTTCTGCTCCTAGTCGTGTACAATCAAATGGCTTCCACCATAGGCGAATGCATCT  
b K K R R G S A H V S L P K V V S A Y V D -

TTTTTATACGAACTTGCAGGAATTGCTGTGCGATGAAGTAACTAGGGCCAGAACCGATAC  
9601 -----+-----+-----+-----+-----+-----+ 9660  
AAAAATATGCTTGAACGTCCTTAACGACAGCCTACTTCATTGATCCCGGTCTTGGCTATG  
b F Y T N L Q E L L S D E V T R A R T D T -

AGTTTCGGCATACGCTACCGACTCTATGGCTTTCTTAGTTAAGATGTTACCCCTGACTGC  
9661 -----+-----+-----+-----+-----+-----+ 9720  
TCAAAGCCGTATGCGATGGCTGAGATACCGAAAGAATCAATTCTACAATGGGGACTGACG  
b V S A Y A T D S M A F L V K M L P L T A -

TCGTGAGCAGTGGTTAAAAGACGTGCTAGGATATCTGCTGGTACGGAGACGACCAGCAAA  
9721 -----+-----+-----+-----+-----+-----+ 9780  
AGCACTCGTCACCAATTTTCTGCACGATCCTATAGACGACCATGCCTCTGCTGGTCTGTTT  
b R E Q W L K D V L G Y L L V R R R P A N -

TTTTTCCTACGACGTAAGAGTAGCTTGGGTATATGACGTGATCGCTACGCTCAAGCTGGT  
9781 -----+-----+-----+-----+-----+-----+ 9840  
AAAAAGGATGCTGCATTCTCATCGAACCCATATACTGCACTAGCGATGCGAGTTCCACCA  
b F S Y D V R V A W V Y D V I A T L K L V -

CATAAGATTGTTTTTCAACAAGGACACACCCGGGGGTATTAAAGACTTAAAACCGTGTGT  
9841 -----+-----+-----+-----+-----+-----+ 9900  
GTATTCTAACA AAAAGTTGTTTCTGTGTGGGCCCCCATAATTTCTGAATTTTGGCACACA  
b I R L F F N K D T P G G I K D L K P C V -

GCCTATAGAGTCATTCGACCCCTTTCACGAGCTTTTCGTCCTATTTCTCTAGGTTAAGTTA  
9901 -----+-----+-----+-----+-----+-----+ 9960  
CGGATATCTCAGTAAGCTGGGGAAAGTGCTCGAAAGCAGGATAAAGAGATCCAATTCAT  
b P I E S F D P F H E L S S Y F S R L S Y -

CGAGATGACGACAGGTAAAGGGGAAAGATATGCCCCGAGATCGCCGAGAAGTTGGTGCG  
9961 -----+-----+-----+-----+-----+-----+ 10020  
GCTCTACTGCTGTCCATTTCCCCCTTTCTATACGGGCTCTAGCGGCTCTTCAACCACGC  
b E M T T G K G G K I C P E I A E K L V R -

CCGTCTAATGGAGGAAAACCTATAAGTTAAGATTGACCCCAGTGATGGCCTTAATAATTAT  
10021 -----+-----+-----+-----+-----+-----+ 10080  
GGCAGATTACCTCCTTTTGATATTCAATTCTAACTGGGGTCACTACCGGAATTATTAATA  
b R L M E E N Y K L R L T P V M A L I I I -

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FIG. 18P

10081 ACTGGTATACTACTCCATTTACGGCACAAACGCTACCAGGATTAAAAGACGCCCCGGATTT  
-----+-----+-----+-----+-----+-----+ 10140  
TGACCATATGATGAGGTAAATGCCGTGTTTGGCATGGTCCTAATTTTCTGCGGGCCTAAA  
b L V Y Y S I Y G T N A T R I K R R P D F -

10141 CCTCAATGTGAGGATAAAGGGAAGAGTCGAGAAGGTTTCGTTACGGGGGGTAGAAGATCG  
-----+-----+-----+-----+-----+-----+ 10200  
GGAGTTACACTCCTATTTCCCTTCTCAGCTCTTCCAAAGCAATGCCCCCATCTTCTAGC  
b L N V R I K G R V E K V S L R G V E D R -

10201 TGCCTTTAGAATATCAGAAAAGCGCGGGATAAACGCTCAACGTGTATTATGTAGGTACTA  
-----+-----+-----+-----+-----+-----+ 10260  
ACGGAAATCTTATAGTCTTTTCGCGCCCTATTTGCGAGTTGCACATAATACATCCATGAT  
b A F R I S E K R G I N A Q R V L C R Y Y -

10261 TAGCGATCTCACATGTCTGGCTAGGCGACATTACGGCATTTCGAGGAACAATTGGAAGAC  
-----+-----+-----+-----+-----+-----+ 10320  
ATCGCTAGAGTGACAGACCGATCCGCTGTAATGCCGTAAGCGTCCTTGTAAACCTTCTG  
b S D L T C L A R R H Y G I R R N N W K T -

10321 GCTGAGTTATGTAGACGGGACGTTAGCGTATGACACGGCTGATTGTATAACTTCTAAGGT  
-----+-----+-----+-----+-----+-----+ 10380  
CGACTCAATACATCTGCCCTGCAATCGCATACTGTGCCGACTAACATATTGAAGATTCCA  
b L S Y V D G T L A Y D T A D C I T S K V -

10381 GAGAAATACGATCAACACCGCAGATCACGCTAGCATTATACACTATATCAAGACGAACGA  
-----+-----+-----+-----+-----+-----+ 10440  
CTCTTTATGCTAGTTGTGGCGTCTAGTGCGATCGTAATATGTGATATAGTTCTGCTTGCT  
b R N T I N T A D H A S I I H Y I K T N E -

10441 AAACCAGGTTACCGGAACTACTCTACCACACCAGCTTTAAAGCTGCGTGTAGTATGCGAC  
-----+-----+-----+-----+-----+-----+ 10500  
TTTGGTCCAATGGCCTTGATGAGATGGTGTGGTCGAAATTTGACGCACATCATACGCTG  
b N Q V T G T T L P H Q L \* -

10501 GATGTTTCTCGTATTAGTTTTATAAAAATTTTTAATTGCTCTGTGTGTGGTTTTTGTGTA  
-----+-----+-----+-----+-----+-----+ 10560  
CTACAAAGAGCATAATCAAAATATTTTTAAAAATTAACGAGACACACACCAAAAACAAC

ORF6 (Coat protein)

10561 GTGAACGCGATGGCATTGAACTGAAATTAGGGCAGATATATGAAGTCGTCCCCGAAAT  
-----+-----+-----+-----+-----+-----+ 10620  
CACTTGCGCTACCGTAAACTTGACTTTAATCCCGTCTATATACTTCAGCAGGGGCTTTTA  
a M A F E L K L G Q I Y E V V P E N -

10621 AATTTGAGAGTTAGAGTGGGGGATGCGGCACAAGGAAAATTTAGTAAGGCGAGTTTCTTA  
-----+-----+-----+-----+-----+-----+ 10680  
TTAAACTCTCAATCTCACCCCTACGCCGTGTTCCCTTTTAAATCATTCGCGCTCAAAGAAT  
a N L R V R V G D A A Q G K F S K A S F L -

10681 AAGTACGTTAAGGACGGGACACAGGCGGAATTAACGGGAATCGCCGTAGTGCCCGAAAAA  
-----+-----+-----+-----+-----+-----+ 10740  
TTCATGCAATTCCCTGCCCTGTGTCCGCCTTAATTGCCCTTAGCGGCATCACGGGCTTTTT  
a K Y V K D G T Q A E L T G I A V V P E K -

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**FIG. 18Q**

10741 TACGTATTTCGCCACAGCAGCTTTGGCTACAGCGGCGCAGGAGCCACCTAGGCAGCCACCA 10800  
-----+-----+-----+-----+-----+-----+  
a ATGCATAAGCGGTGTCGTCGAAACCGATGTCGCCGCGTCCTCGGTGGATCCGTCGGTGGT  
Y V F A T A A L A T A A Q E P P R Q P P -  
  
10801 GCGCAAGTGGCGGAACCACAGGAAACCGATATAGGGGTAGTGCCGGAATCTGAGACTCTC 10860  
-----+-----+-----+-----+-----+-----+  
a CGCGTTACCGCCTTGGTGTCTTTGGCTATATCCCCATCACGGCCTTAGACTCTGAGAG  
A Q V A E P Q E T D I G V V P E S E T L -  
  
10861 ACACCAAATAAGTTGGTTTTTCGAGAAAGATCCAGACAAGTTCTTGAAGACTATGGGCAAG 10920  
-----+-----+-----+-----+-----+-----+  
a TGTGGTTTATTCAACCAAAGCTCTTTCTAGGTCTGTTCAAGAACTTCTGATACCCGTTT  
T P N K L V F E K D P D K F L K T M G K -  
  
10921 GGAATAGCTTTGGACTTGGCGGGAGTTACCCACAAACCGAAAGTTATTAACGAGCCAGGG 10980  
-----+-----+-----+-----+-----+-----+  
a CCTTATCGAAACCTGAACCGCCCTCAATGGGTGTTTGGCTTTCAATAATTGCTCGGTCCC  
G I A L D L A G V T H K P K V I N E P G -  
  
10981 AAAGTATCAGTAGAGGTGGCAATGAAGATTAATGCCGCATTGATGGAGCTGTGTAAGAAG 11040  
-----+-----+-----+-----+-----+-----+  
a TTTCATAGTCATCTCCACCGTTACTTCTAATTACGGCGTAACTACCTCGACACATTCTTC  
K V S V E V A M K I N A A L M E L C K K -  
  
11041 GTTATGGGCGCCGATGACGCAGCAACTAAGACAGAATTCTTCTTGTACGTGATGCAGATT 11100  
-----+-----+-----+-----+-----+-----+  
a CAATACCCGCGGCTACTGCGTCGTTGATTCTGTCTTAAGAAGAACATGCACTACGTCTAA  
V M G A D D A A T K T E F F L Y V M Q I -  
  
11101 GCTTGACGTTCTTTACATCGTCTTCGACGGAGTTCAAAGAGTTTGACTACATAGAAACC 11160  
-----+-----+-----+-----+-----+-----+  
a CGAACGTGCAAGAAATGTAGCAGAAGCTGCCTCAAGTTTCTCAAACCTGATGTATCTTTGG  
A C T F F T S S S T E F K E F D Y I E T -  
  
11161 GATGATGGAAAGAAGATATATGCGGTGTGGGTATATGATTGCATTAAACAAGCTGCTGCT 11220  
-----+-----+-----+-----+-----+-----+  
a CTACTACCTTTCTTCTATATACGCCACACCCATATACTAACGTAATTTGTTGACGACGA  
D D G K K I Y A V W V Y D C I K Q A A A -  
  
11221 TCGACGGGTTATGAAAACCCGGTAAGGCAGTATCTAGCGTACTTCACACCAACCTTCATC 11280  
-----+-----+-----+-----+-----+-----+  
a AGCTGCCCAATACTTTTGGGCCATTCCGTCATAGATCGCATGAAGTGTGGTTGGAAGTAG  
S T G Y E N P V R Q Y L A Y F T P T F I -  
  
11281 ACGGCGACCCTGAATGGTAAACTAGTGATGAACGAGAAGGTTATGGCACAGCATGGAGTA 11340  
-----+-----+-----+-----+-----+-----+  
a TGCCGCTGGGACTTACCATTTGATCACTACTTGCTCTTCCAATACCGTGTCTGACCTCAT  
T A T L N G K L V M N E K V M A Q H G V -  
  
11341 CCACCGAAATTCTTTCCGTACACGATAGACTGCGTTTCGTCCGACGTACGATCTGTTCAAC 11400  
-----+-----+-----+-----+-----+-----+  
a GGTGGCTTTAAGAAAGGCATGTGCTATCTGACGCAAGCAGGCTGCATGCTAGACAAGTTG  
P P K F F P Y T I D C V R P T Y D L F N -

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**FIG. 18R**

11401 AACGACGCAATATTAGCATGGAATTTAGCTAGACAGCAGGCGTTTAGAAACAAGACGGTA 11460  
-----+-----+-----+-----+-----+-----+  
a TTGCTGCGTTATAATCGTACCTTAAATCGATCTGTCTCCGCAAATCTTTGTTCTGCCAT  
N D A I L A W N L A R Q Q A F R N K T V -

11461 ACGGCCGATAACACCTTACACAACGTCTTCCAACCTATTGCAAAAGAAGTAGCTACGATCG 11520  
-----+-----+-----+-----+-----+-----+  
a TGCCGGCTATTGTGGAATGTGTTGCAGAAGGTTGATAACGTTTTCTTCATCGATGCTAGC  
T A D N T L H N V F Q L L Q K K \* -

11521 ATGTCTATAAATTGGTGAAAAATTTAGAAATATTTACCTTTTATTGATAATTCATGGGAG 11580  
-----+-----+-----+-----+-----+-----+  
a TACAGATATTTAACCACCTTTTAAATCTTTATAAATGAAAAATACTATTAAGTACCCCTC  
M S I N W \* -  
c M G A -

11581 CTTATACACATGTAGACTTTTCATGAGTCGCGGTTGCTGAAAGACAAACAAGACTATCTTT 11640  
-----+-----+-----+-----+-----+-----+  
c GAATATGTGTACATCTGAAAGTACTCAGCGCCAACGACTTTCTGTTTGTCTGATAGAAA  
Y T H V D F H E S R L L K D K Q D Y L S -

11641 CTTTCAAGTCAGCGGATGAAGCTCCTCCTGATCCTCCCGGATACGTTTCGCCCAGATAGTT 11700  
-----+-----+-----+-----+-----+-----+  
c GAAAGTTCACTCGCCTACTTCGAGGAGGACTAGGAGGGCCTATGCAAGCGGGTCTATCAA  
F K S A D E A P P D P P G Y V R P D S Y -

11701 ATGTGAGGGCTTATTTGATACAAAGAGCAGACTTTCCCAATACTCAAAGCTTATCAGTTA 11760  
-----+-----+-----+-----+-----+-----+  
c TACACTCCCGAATAAACTATGTTTCTCGTCTGAAAGGGTTATGAGTTTCGAATAGTCAAT  
V R A Y L I Q R A D F P N T Q S L S V T -

11761 CGTTATCGATAGCCAGTAATAAGTTAGCTTCAGGTCTTATGGAAGCGACGCAGTATCAT 11820  
-----+-----+-----+-----+-----+-----+  
c GCAATAGCTATCGGTCATTATTCAATCGAAGTCCAGAATACCCCTTCGCTGCGTCATAGTA  
L S I A S N K L A S G L M G S D A V S S -

11821 CGTCGTTTATGCTGATGAACGACGTGGGAGATTACTTCGAGTGCGGCGTGTGTCACAACA 11880  
-----+-----+-----+-----+-----+-----+  
c GCAGCAAATACGACTACTTGCTGCACCCTCTAATGAAGCTCACGCCGCACACAGTGTTGT  
S F M-L M-N-D V G D Y F E C G V C H N K -

11881 AACCCTACTTAGGACGGGAAGTTATCTTCTGTAGGAAATACATAGGTGGGAGAGGAGTGG 11940  
-----+-----+-----+-----+-----+-----+  
c TTGGGATGAATCCTGCCCTTCAATAGAAGACATCCTTTATGTATCCACCCTCTCCTCACC  
P Y L G R E V I F C R K Y I G G R G V E -

11941 AGATCACCCTGGTAAGAACTACACGTCGAACAATTGGAACGAGGCGTCGTACGTAATAC 12000  
-----+-----+-----+-----+-----+-----+  
c TCTAGTGGTGACCATCTTGATGTGCAGCTTGTTAACCTTGCTCCGCAGCATGCATTATG  
I T T G K N Y T S N N W N E A S Y V I Q -

12001 AAGTGAACGTAGTCGATGGGTTAGCACAGACCACTGTTAATTCTACTTATACGCAAACGG 12060  
-----+-----+-----+-----+-----+-----+  
c TTCCTTGCATCAGCTACCCAATCGTGTCTGGTGACAATTAAGATGAATATGCGTTTGCC  
V N V V D G L A Q T T V N S T Y T Q T D -

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FIG. 18S

12061 ACGTTAGTGGTCTACCCAAAAATTGGACGCGTATCTACAAAATAACAAAGATAGTGTCCG  
-----+-----+-----+-----+-----+-----+ 12120  
TGCAATCACCAGATGGGTTTTTAACCTGCGCATAGATGTTTTATTGTTTCTATCACAGGC  
c V S G L P K N W T R I Y K I T K I V S V -

12121 TAGATCAGAACCTCTACCCTGGTTGTTTCTCAGACTCGAAACTGGGTGTAATGCGTATAA  
-----+-----+-----+-----+-----+-----+ 12180  
ATCTAGTCTTGGAGATGGGACCAACAAAGAGTCTGAGCTTTGACCCACATTACGCATATT  
c D Q N L Y P G C F S D S K L G V M R I R -

12181 GGTCACGTGTTAGTTTCCCCAGTGCGCATCTTCTTTAGGGATATCTTATTGAAACCTTTGA  
-----+-----+-----+-----+-----+-----+ 12240  
-CCAGTGACAATCAAAGGGGTACGCGTAGAAGAAATCCCTATAGAATAACTTTGGAAACT  
c S L L V S P V R I F F R D I L L K P L K -

12241 AGAAATCGTTCAACGCAAGAATCGAGGATGTGCTGAATATTGACGACACGTCGTTGTTAG  
-----+-----+-----+-----+-----+-----+ 12300  
TCTTTAGCAAGTTGCGTTCTTAGCTCCTACAGACTTATAACTGCTGTGCAGCAACAATC  
c K S F N A R I E D V L N I D D T S L L V -

12301 TACCGAGTCCTGTGCTACCAGAGTCTACGGGAGGTGTAGGTCCATCAGAGCAGCTGGATG  
-----+-----+-----+-----+-----+-----+ 12360  
ATGGCTCAGGACAGCATGGTCTCAGATGCCCTCCACATCCAGGTAGTCTCGTCGACCTAC  
c P S P V V P E S T G G V G P S E Q L D V -

12361 TAGTGGCTTTAACGTCCGACGTAACGGAATTGATCAACACTAGGGGGCAAGGTAAGATAT  
-----+-----+-----+-----+-----+-----+ 12420  
ATCACCAGAAATTGCAGGCTGCATTGCCTTAAGTAGTTGTGATCCCCGTTCCATTCTATA  
c V A L T S D V T E L I N T R G Q G K I C -

12421 GTTTTCCAGACTCAGTGTATCGATCAATGAAGCGGATATCTACGATGAGCGGTATTTGC  
-----+-----+-----+-----+-----+-----+ 12480  
CAAAAGGTCTGAGTCACAATAGCTAGTTACTTCGCCTATAGATGCTACTCGCCATAAACG  
c F P D S V L S I N E A D I Y D E R Y L P -

12481 CGATAACGGAAGCTCTACAGATAAACGCAAGACTACGCAGACTCGTTCTTTGAAAGGCG  
-----+-----+-----+-----+-----+-----+ 12540  
GCTATTGCCTTCGAGATGTCTATTTGCGTTCTGATGCGTCTGAGCAAGAAAGCTTTCCGC  
c I T E A L Q I N A R L R R L V L S K G G -

12541 GGAGTCAAACACCACGAGATATGGGGAATATGATAGTGGCCATGATACAACCTTTTCGTAC  
-----+-----+-----+-----+-----+-----+ 12600  
CCTCAGTTTGTGGTGCTCTATACCCCTTATACTATCACCAGTACTATGTTGAAAAGCATG  
c S Q T P R D M G N M I V A M I Q L F V L -

12601 TCTACTCTACTGTAAAGAATATAAGCGTCAAAGACGGGTATAGGGTGGAGACCGAATTAG  
-----+-----+-----+-----+-----+-----+ 12660  
AGATGAGATGACATTTCTTATATTTCGCAGTTTCTGCCCATATCCCACCTCTGGCTTAATC  
c Y S T V K N I S V K D G Y R V E T E L G -

12661 GTCAAAGAGAGTCTACTTAAGTTATTCCGGAAGTAAGGGAAGCTATATTAGGAGGGAAAT  
-----+-----+-----+-----+-----+-----+ 12720  
CAGTTTTCTCTCAGATGAATTCAATAAGCCTTCATTCCCTTCGATATAATCCTCCCTTTA  
c Q K R V Y L S Y S E V R E A I L G G K Y -

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FIG. 18T

ACGGTGCGTCTCCAACCAACACTGTGCGATCCTTCATGAGGTATTTTGCTCACACCACTA  
12721 -----+-----+-----+-----+-----+-----+ 12780  
TGCCACGCAGAGGTTGGTTGTGACACGCTAGGAAGTACTCCATAAAACGAGTGTGGTGAT  
c G A S P T N T V R S F M R Y F A H T T I -  
  
TTACTCTACTTATAGAGAAGAAAATTCAGCCAGCGTGTACTGCCCTAGCTAAGCACGGCG  
12781 -----+-----+-----+-----+-----+-----+ 12840  
AATGAGATGAATATCTCTTTTAAAGTCGGTCGCACATGACGGGATCGATTTCGTGCCGC  
c T L L I E K K I Q P A C T A L A K H G V -  
  
TCCCGAAGAGGTTCACTCCGTACTGCTTCGACTTCGCACTACTGGATAACAGATATTACC  
12841 -----+-----+-----+-----+-----+-----+ 12900  
AGGGCTTCTCCAAGTGAGGCATGACGAAGCTGAAGCGTGATGACCTATTGTCTATAATGG  
c P K R F T P Y C F D F A L L D N R Y Y P -  
  
CGGCGGACGTGTTGAAGGCTAACGCAATGGCTTGCGCTATAGCGATTAAATCAGCTAATT  
12901 -----+-----+-----+-----+-----+-----+ 12960  
GCCGCCTGCACAACTTCCGATTGCGTTACCGAACCGGATATCGCTAATTTAGTCGATTAA  
c A D V L K A N A M A C A I A I K S A N L -  
  
ORF8  
TAAGGCGTAAAGGTTCCGAGACGTATAACATCTTAGAAAGCATTTGATTATCTAAAGATG  
12961 -----+-----+-----+-----+-----+-----+ 13020  
ATTCCGCATTTCCAAGCCTCTGCATATTGTAGAATCTTTCGTAAACTAATAGATTTCTAC  
a M -  
c R R K G S E T Y N I L E S I \* -  
  
GAATTCAGACCAGTTTAAATTACAGTTCCCGTGATCCCGGCGTAAACACTGGTAGTTTG  
13021 -----+-----+-----+-----+-----+-----+ 13080  
CTTAAGTCTGGTCAAAATTAATGTCAAGCGGCACTAGGGCCGCATTTGTGACCATCAAAC  
a E F R P V L I T V R R D P G V N T G S L -  
  
AAAGTGATAGCTTATGACTTACACTACGACAATATATTCGATAACTGCGCGGTAAAGTCG  
13081 -----+-----+-----+-----+-----+-----+ 13140  
TTTCACTATCGAATACTGAATGTGATGCTGTTATATAAGCTATTGACGCGCCATTTTCAGC  
a K V I A Y D L H Y D N I F D N C A V K S -  
  
TTTCGAGACACCGACACTGGATTCACTGTTATGAAAGAATACTCGACGAATTCAGCGTTC  
13141 -----+-----+-----+-----+-----+-----+ 13200  
AAAGCTCTGTGGCTGTGACCTAAGTGACAATACTTTCTTATGAGCTGCTTAAGTCGCAAG  
a F R D T D T G F T V M K E Y S T N S A F -  
  
ATACTAAGTCCTTATAAACTGTTTCCGCGGTCTTTAATAAGGAAGGTGAGATGATAAGT  
13201 -----+-----+-----+-----+-----+-----+ 13260  
TATGATTCAGGAATATTTGACAAAAGGCGCCAGAAATTATTCCTTCCACTCTACTATTCA  
a I L S P Y K L F S A V F N K E G E M I S -  
  
AACGATGTAGGATCGAGTTTCAGGGTTTACAATATCTTTTCGCAAATGTGTAAAGATATC  
13261 -----+-----+-----+-----+-----+-----+ 13320  
TTGCTACATCCTAGCTCAAAGTCCCAAATGTTATAGAAAAGCGTTTACACATTTCTATAG  
a N D V G S S F R V Y N I F S Q M C K D I -  
  
AACGAGATCAGCGAGATACAACGCGCCGGTTACCTAGAAACATATTTAGGAGACGGGCAG  
13321 -----+-----+-----+-----+-----+-----+ 13380  
TTGCTCTAGTCGCTCTATGTTGCGCGGCCAATGGATCTTTGTATAAATCCTCTGCCCGTC  
a N E I S E I Q R A G Y L E T Y L G D G Q -

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FIG. 18U

13381 GCTGACACTGATATATTTTTTGTATGCTTAACCAACAACAAAGCAAAGGTAAGGTGGTTA  
-----+-----+-----+-----+-----+ 13440  
CGACTGTGACTATATAAAAACTACAGAATTGGTTGTTGTTTCGTTTCCATTCCACCAAT  
a A D T D I F F D V L T N N K A K V R W L -

13441 GTTAATAAAGACCATAGCGCGTGGTGTGGGATATTGAATGATTTGAAGTGGGAAGAGAGC  
-----+-----+-----+-----+-----+ 13500  
CAATTATTTCTGGTATCGCGCACCACACCCTATAACTTACTAACTTCACCCTTCTCTCG  
a V N K D H S A W C G I L N D L K W E E S -

13501 AACAAGGAGAAATTTAAGGGGAGAGACATACTAGATACTTACGTTTTATCGTCTGATTAT  
-----+-----+-----+-----+-----+ 13560  
TTGTTCTCTTTAAATTTCCCTCTCTGTATGATCTATGAATGCAAATAGCAGACTAATA  
a N K E K F K G R D I L D T Y V L S S D Y -

ORF9

13561 CCAGGGTTTAAATGAAGTTGCTTTTCGCTCCGCTATCTTATCTTAAGGTTGTCAAAGTCGC  
-----+-----+-----+-----+-----+ 13620  
GGTCCCAAATTTACTTCAACGAAAGCGAGGCGATAGAATAGAATTCCAACAGTTTCAGCG  
a P G F K \*  
c M K L L S L R Y L I L R L S K S L -

13621 TTAGAACGAACGATCACTTGGTTTTAATACTTATAAAGGAGGCGCTTATAAACTATTACA  
-----+-----+-----+-----+-----+ 13680  
AATCTTGCTTGCTAGTGAACCAAAATTATGAATATTTCTCCGGAATATTTGATAATGT  
c R T N D H L V L I L I K E A L I N Y Y N -

13681 ACGCCTCTTTTACCGATGAGGGTGCCGTATTAAGAGACTCTCGCGAAAGTATAGAGAATT  
-----+-----+-----+-----+-----+ 13740  
TGCGGAGAAAGTGGCTACTCCACGGCATAATTCTCTGAGAGCGCTTTCATATCTCTTAA  
c A S F T D E G A V L R D S R E S I E N F -

13741 TTCTCGTAGCCAGGTGCGGTTTCGCAAATTCCTGCCGAGTCATGAAGGCTTTGATCACTA  
-----+-----+-----+-----+-----+ 13800  
AAGAGCATCGGTCCACGCCAAGCGTTTTAAGGACGGCTCAGTACTTCCGAACTAGTGAT  
c L V A R C G S Q N S C R V M K A L I T N -

13801 ACACAGTCTGTAAGATGTCGATAGAAACAGCCAGAAGTTTTATCGGAGACTTAATACTCG  
-----+-----+-----+-----+-----+ 13860  
TGTGTCAGACATTCTACAGCTATCTTTGTGCGTCTTCAAATAGCCTCTGAATTATGAGC  
c T V C K M S I E T A R S F I G D L I L V -

13861 TCGCCGACTCCTCTGTTTCAGCGTTGGAAGAAGCGAAATCAATTAAAGATAATTTCCGCT  
-----+-----+-----+-----+-----+ 13920  
AGCGGCTGAGGAGACAAAGTCGCAACCTTCTTCGCTTTAGTTAATTTCTATTAAAGGCGA  
c A D S S V S A L E E A K S I K D N F R L -

13921 TAAGAAAAAGGAGAGGCAAGTATTATTATAGTGGTGATTGTGGATCCGACGTTGCCGAAAG  
-----+-----+-----+-----+-----+ 13980  
ATTCTTTTTCTCTCCGTTTATAATAATATCACCCTAACACCTAGGCTGCAACGCTTTC  
c R K R R G K Y Y Y S G D C G S D V A K V -

13981 TTAAGTATATTTTGTCTGGGGAGAATCGAGGATTGGGGTGCGTAGATTCCCTTGAAGCTAG  
-----+-----+-----+-----+-----+ 14040  
AATTCATATAAAACAGACCCCTCTTAGCTCCTAACCCACGCATCTAAGGAACCTTCGATC  
c K Y I L S G E N R G L G C V D S L K L V -

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FIG. 18V

14041 TTTGCGTAGGTAGACAAGGAGGTGGAACGTACTACAGCACCTACTAATCTCATCTCTGG  
-----+-----+-----+-----+-----+-----+ 14100  
AAACGCATCCATCTGTTCCCTCCACCTTTGCATGATGTCGTGGATGATTAGAGTAGAGACC  
C V G R Q G G G N V L Q H L L I S S L G -

ORF10

14101 GTTAAAGCATCATGGACCTATCGTTTATTATTGTGCAGATCCTTTCCGCCTCGTACAATA  
-----+-----+-----+-----+-----+-----+ 14160  
CAATTTTCGTAGTACCTGGATAGCAAATAATAACACGTCTAGGAAAGGCGGAGCATGTTAT  
\* M D L S F I I V Q I L S A S Y N N -

14161 ATGACGTGACAGCACTTTACACTTTGATTAACGCGTATAATAGCGTTGATGATACGACGC  
-----+-----+-----+-----+-----+-----+ 14220  
TACTGCACTGTCGTGAAATGTGAAACTAATTGCGCATATTATCGCAACTACTATGCTGCG  
D V T A L Y T L I N A Y N S V D D T T R -

14221 GCTGGGCAGCGATAAACGATCCGCAAGCTGAGGTTAACGTCGTGAAGGCTTACGTAGCTA  
-----+-----+-----+-----+-----+-----+ 14280  
CGACCCGTCGCTATTTGCTAGGCGTTGCACTCCAATTGCAGCACTTCCGAATGCATCGAT  
W A A I N D P Q A E V N V V K A Y V A T -

14281 CTACAGCGACGACTGAGCTGCATAGAACAATTCTCATTGACAGTATAGACTCCGCCTTCG  
-----+-----+-----+-----+-----+-----+ 14340  
GATGTCGTGCTGACTCGACGTATCTTGTAAAGAGTAAGTGTATATCTGAGGCGGAAGC  
T A T T E L H R T I L I D S I D S A F A -

14341 CTTATGACCAAGTGGGGTGTGTTGGTGGGCATAGCTAGAGGTTTGCTTAGACATTCCGAAG  
-----+-----+-----+-----+-----+-----+ 14400  
GAATACTGGTTTCACCCACAAACCACCCGTATCGATCTCCAAACGAATCTGTAAGCCTTC  
Y D Q V G C L V G I A R G L L R H S E D -

14401 ATGTTCTGGAGGTCATCAAGTCGATGGAGTTATTGCAAGTGTGTCGTGGAAAGAGGGGAA  
-----+-----+-----+-----+-----+-----+ 14460  
TACAAGACCTCCAGTAGTTCAGCTACCTCAATAAGCTTCACACAGCACCTTTCTCCCCTT  
V L E V I K S M E L F E V C R G K R G S -

14461 GCAAAAGATATCTTGGATACTTAAGTGATCAATGCACTAACAATAACATGATGCTAACTC  
-----+-----+-----+-----+-----+-----+ 14520  
CGTTTTCTATAGAACCTATGAATTCAGTACGTGATTGTTTATGTACTACGATTGAG  
K R Y L G Y L S D Q C T N K Y M M L T Q -

14521 AGGCCGGACTGGCCGCACTTGAAGGAGCAGACATACTACGAACGAATCATCTAGTCAGTG  
-----+-----+-----+-----+-----+-----+ 14580  
TCCGGCCTGACCGGCGTCAACTTCCTCGTCTGTATGATGCTTGCTTAGTAGATCAGTCAC  
A G L A A V E G A D I L R T N H L V S G -

14581 GTAATAAGTTCTCTCCAAATTTCCGGATCGCTAGGATGTTGCTCTTGACGCTTTGTTGCG  
-----+-----+-----+-----+-----+-----+ 14640  
CATTATTCAAGAGAGGTTTAAAGCCCTAGCGATCCTACAACGAGAACTGCGAAACAACGC  
N K F S P N F G I A R M L L L T L C C G -

14641 GAGCACTATAAAAAATGTTATGTTGTTTCAGCCAGTGTCAAATTTTCAAACGGGTTACAATT  
-----+-----+-----+-----+-----+-----+ 14700  
CTCGTGATATTTTACAATACAACAAGTCGGTCACAGTTTAAAAGTTTGCCCAATGTTAA  
A L \*



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**FIG. 18W**

14701 ATCGCTACTTATTTGCGCATGTTTGTTAGCGGTGCTAATTGTTAGCTTTTGTAGAAGGCG  
-----+-----+-----+-----+-----+ 14760  
TAGCGATGAATAAACGCGTACAAACAATCGCCACGATTAACAATCGAAAACATCTTCCGC

**ORF11**

14761 ATGAGGCACTTAGAAAAACCCATCAGAGTAGCGGTACACTATTGCGTCGTGCGAAGTGAC  
-----+-----+-----+-----+-----+ 14820  
TACTCCGTGAATCTTTTTGGGTAGTCTCATCGCCATGTGATAACGCAGCACGCTTCACTG  
a M R H L E K P I R V A V H Y C V V R S D -

14821 GTTTGTGACGGGTGGGATGTATTTATAGGCGTAACGTTAATCGGTATGTTTATTAGTTAC  
-----+-----+-----+-----+-----+ 14880  
CAAACACTGCCCACCCTACATAAATATCCGCATTGCAATTAGCCATACAAATAATCAATG  
a V C D G W D V F I G V T L I G M F I S Y -

14881 TATTTATATGCTCTAATTAGCATATGTAGAAAAGGAGAAGGTTTAACAACCAGTAATGGG  
-----+-----+-----+-----+-----+ 14940  
ATAAATATACGAGATTAATCGTATACATCTTTTCCTCTTCCAAATTGTTGGTCATTACCC  
a Y L Y A L I S I C R K G E G L T T S N G -

14941 TAAAAATCCTTCAATAAATTTGAAATAAACAAAAGTAAGAAAAATGAAATAATTAGGCTA  
-----+-----+-----+-----+-----+ 15000  
ATTTTTAGGAAGTTATTTAACTTTATTTGTTTTCATTCTTTTACTTTATTAATCCGAT  
a \* -

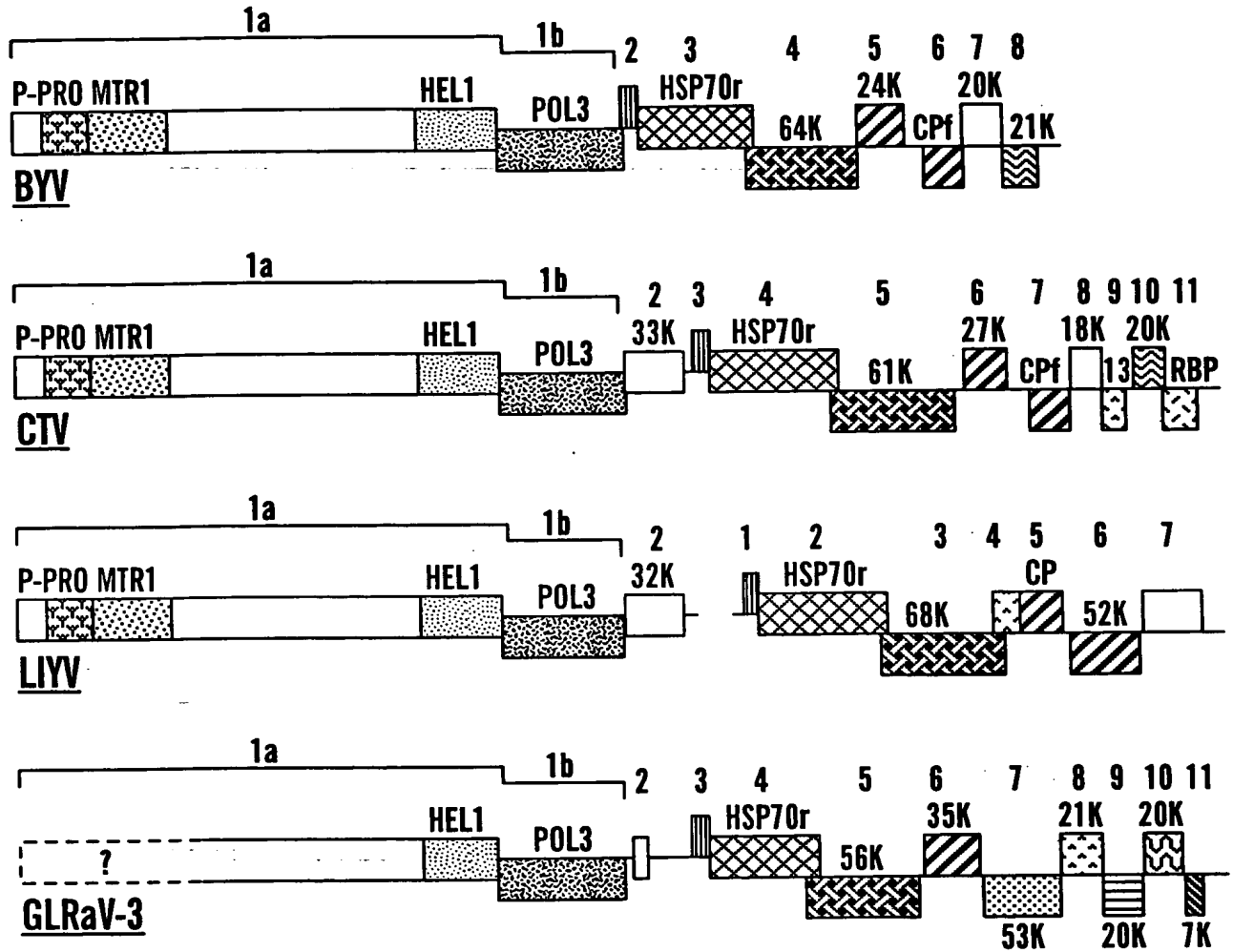
15001 GTCTTTTTGTTTCGTCTTTTCGCTTTTGTAGAATAGGTTTATTTTCGAGGTAAGATGACTAA  
-----+-----+-----+-----+-----+ 15060  
CAGAAAAACAAGCAGAAAGCGAAAACATCTTATCCAAAATAAAGCTCCATTCTACTGATT

15061 ACTCTACCTCACGGTTTAATACTCTGATATTTGTAAAAATTAGTCCGTAAAGTCAGATAGT  
-----+-----+-----+-----+-----+ 15120  
TGAGATGGAGTGCCAAATTATGAGACTATAAACATTTTAATCAGGCATTTCACTCTATCA

15121 GATATTATATTAGTATAGTATAATAAACGCCAAAATCCAATCAAAGTTTGGGACCTAGGC  
-----+-----+-----+-----+-----+ 15180  
CTATAATATAATCATATCATATTATTTGCGGTTTATAGGTTAGTTTCAAACCCTGGATCCG

15181 GGGCCTCTTATGAGGCTAACTTATCGACAATAAGTTAGGTCCGCCAC  
-----+-----+-----+-----+ 15227  
CCCGGAGAATACTCCGATTGAATAGCTGTTATTCATCCAGGCGGTG

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**FIG. 19**

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FIG. 20

	I (A)				Ia	
BYV_HEL	FTFTNLSANV	LLYEAPPGGG	KTTTTLIKVFC	ETFSK.VNSL	ILTANKSSRE	
CTV_HEL	LTFTNEEHS	IVYEAPPGGG	KTHSLVNSYA	DYCVK.VSCL	VVTANKNSQT	
GLRaV3_HEL	VGESFKSFEY	KCYNAPPGGG	KTT...MLV	DEFVKSPNST	ATITANVGSS	
LIYV_HEL	MVRRPDVNG	KFYNKPPGAG	KTTTIAKLMS	KDLKNKVKCL	ALSYTKVGRL	
CONSENSUS	-----	--Y-aPPGaG	KTt-----	d-f-k-v--l	-----k----	

	II				
BYV_HEL	EILAKVNRIV	LD...EGDTP	LQTRDRILTI	DSYLMNNR.G	LTCKVLYLDE
CTV_HEL	EISQRISNEL	MGRKLAAYV	TDAASRVFTV	DSYLMNHL.R	LTQQLLFIDE
GLRaV3_HEL	EDINM....A	VKKR...DPN	LEGLNSATTV	NSRVVNFIVR	GMVKRVLVDE
LIYV_HEL	ELIDKLKKDG	IEKP...EKY	VKTYDSFLMN	NDNILEIV..	....NLYCDE
CONSENSUS	E-----	-----d--	-----ltv	-s--mn----	-----ly-DE

	III				
BYV_HEL	CFMVHAGAAV	ACIEFTKCD	AILFGDSRQI	RYGRCSLDT	AVLSDLNRFV
CTV_HEL	CFMVHAGAIG	AVVEFTSCKA	VVFFGDSKQI	HYIHRNDLGV	SFVADIDAFI
GLRaV3_HEL	VYMMHQG.LL	QLGVFQPA	GLFFGDINQI	PFINREKVFR	MDCA..VXLP
LIYV_HEL	VFMMHAGHFL	TLLTKIAYQN	GYCYGDVNQI	PFINRDPYTP	AYLS..REFF
CONSENSUS	-fM-HaG---	----f--c--	--ffGD--QI	--i-r-----	-----f-

	IV				
BYV_HEL	DDESRVYGEV	SYRCPWDVCA	WLSTF.....	...YPKTVAT	TNLVSAGQSS
CTV_HEL	QPEHRIYGEV	SYRCPWDICE	WLSEF.....	...YPRH VAT	ANVGSIGKSS
GLRaV3_HEL	KKESVVYTSK	SYRCPDVCY	LLSSMTVRGT	EKCYPEKVVS	GKDK.PVVR
LIYV_HEL	RKQDLNYDTY	TYRCPDTCY	LLSNLKDEMG	NIIYAGGVKN	VNEVYPTIRS
CONSENSUS	--e--vY---	SYRCP-DvC-	-LS-f-----	---Yp--V--	-n-----S

	V				
BYV_HEL	MQVREIESVD	DVEYSSEFVY	LTMLQSEKGD	LLKSFGK..R	SRSSVEKPTV
CTV_HEL	VSIEEINGCD	DVPYDKAAKY	IVYTQAEKND	LQKHLGRLLTV	GRNKV.VPIV
GLRaV3_HEL	LSKRPIGTTD	DVAEINADV	LCMTQLEKSD	MKRSKLGKGG	.ETP.....V
LIYV_HEL	LNLFGINVVG	EVPVEYNAKY	LTFTQDEKLN	LQRHIDSQGG	CRNA.....V
CONSENSUS	l----I---d	dV-----Y	l--tQ-EK-d	l---l-----	-r-----V

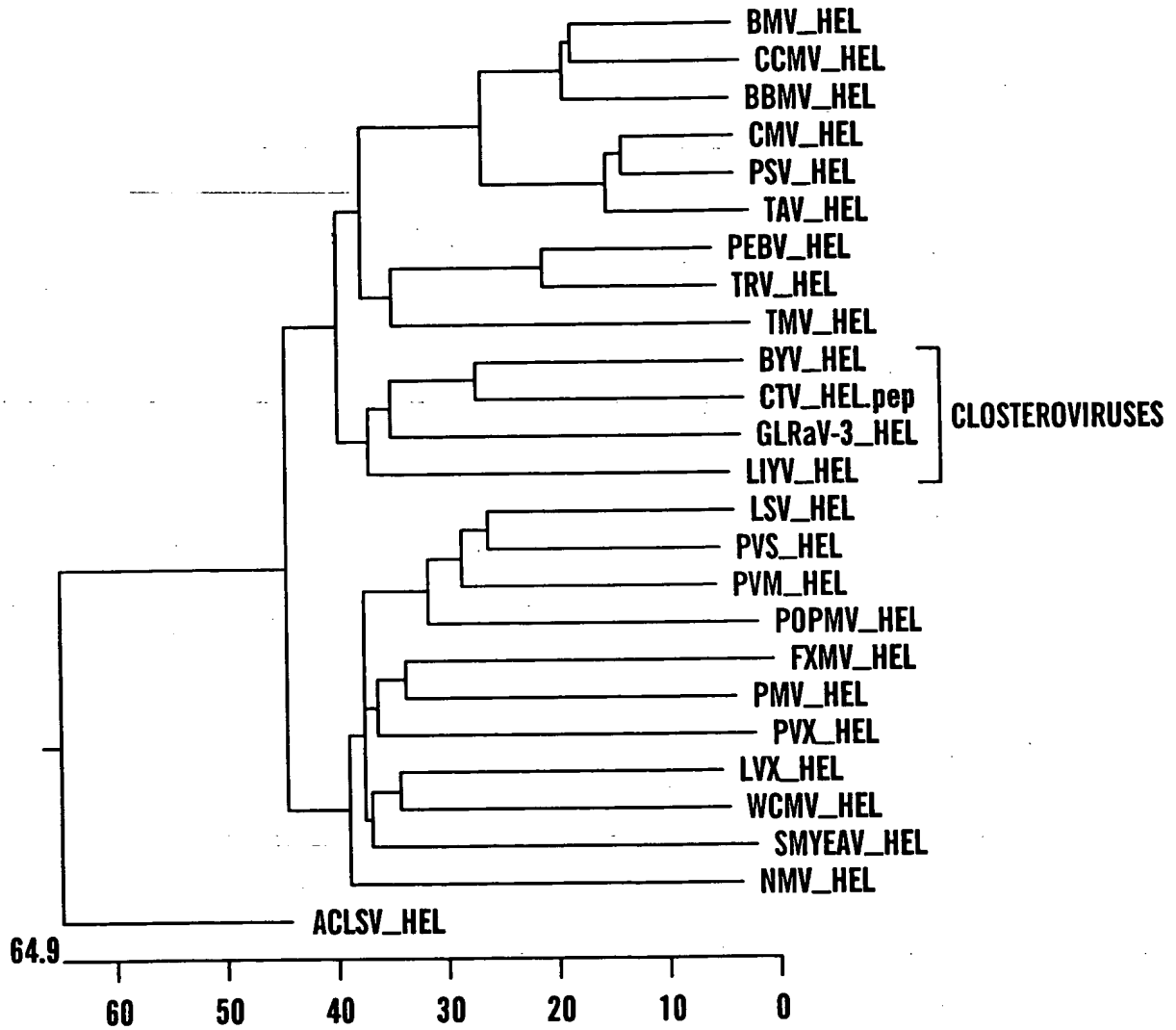
  

	VI				
BYV_HEL	LTVHEAQGET	YRKVNLRVTK	FQEDDPFRSE	NHITVALSRH	VESLTYSVLS
CTV_HEL	NTVHEVQGET	YKRVRLVRFK	YQEDTPFSSK	NHIVVALTRH	VDSLVSVLTV
GLRaV3_HEL	MTVHEAQGKT	FSDVVLFR TK	KADDSLFTKQ	PHILVGLSRH	TRSLVYAALS
LIYV_HEL	STVNEAQGCT	FSEVNLVRLV	QFDNPVMSDI	NQFVVAISRH	TTTFKYFTPH
CONSENSUS	-TVhEaQG-T	---V-LvR-k	---d--f---	nhi-ValsRH	--sl-Y--l-

BYV_HEL	SKRDDAIAQA	I
CTV_HEL	SRRYDDTATN	I
GLRaV3_HEL	SELDDKVGTY	I
LIYV_HEL	SRLNDRVSNA	I
CONSENSUS	S---D-v---	I

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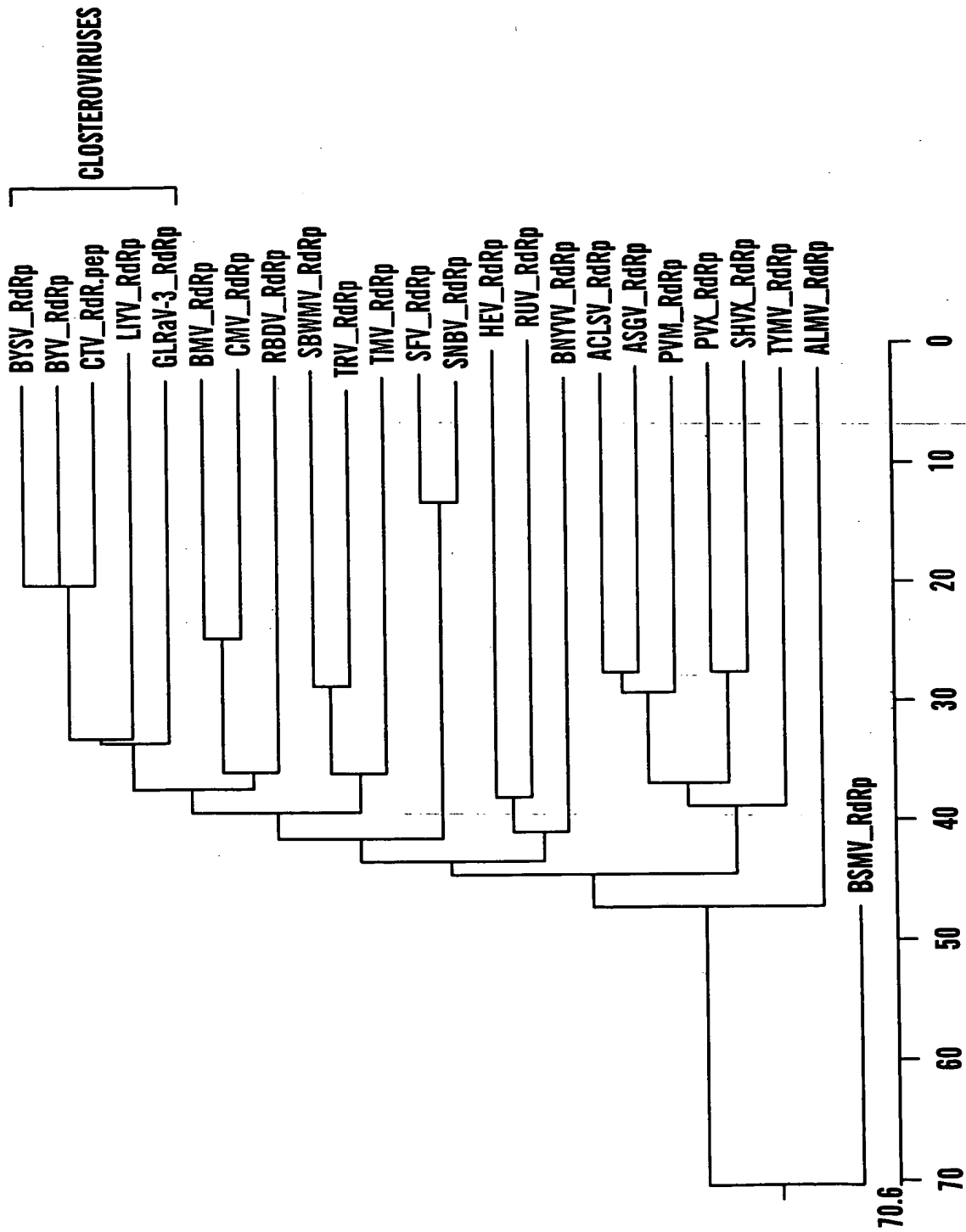
**FIG. 21**

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FIG. 22

	I		II	
BYV_RdRp	ITTFKLMVKR	DAKVKLDSSC	LVKHPPAQNI	MFHRKAVNAI
CTV_RdRp	ISNFKLMVKR	DAKVKLDDSS	LSKHPPAQNI	MFHKKFINAI
GLRaV3_RdRp	LTSYTLMVKA	DVKPKLDNTP	LSKYVTGQNI	VYHRCVTAL
LIYV_RdRp	FKTLNLMVKG	ETKPKMDLST	YDSYNAPANI	VYYQQIVNLY
CONSENSUS	---	f-LMVK- d-K-KlD-s- l-k----	qNI --h---vna-	FSp-F-e---
	III		IV	
BYV_RdRp	RVITCTNSNI	VFFTEMTNST	LASIAKEMLG	.SEHVYNVGE
CTV_RdRp	RVLSSLNDNI	VFFTEMTNAG	LAEIIRRIIG	.DDDNLFVGE
GLRaV3_RdRp	RLKYVVDERW	LFYHGMDTAE	LAXALRNNLG	.DIRQYYTYE
LIYV_RdRp	RLTYCLSDKI	VLYSGMNTDV	LAELIESKLP	LGLNAYHTLE
CONSENSUS	R-----d-i	vf---M----	LA-----lg	-----y---E idfSKfDKSQ
BYV_RdRp	DAFIKSFERT	LYSAFGFDED	LLD.VWMOGE	YTSNATTLDG
CTV_RdRp	DLFIKEYERT	LYSEFGFDTE	LLD.VWMEGE	YRARATTLDG
GLRaV3_RdRp	SALMKQVEEL	ILLTLGVDRE	VLS.TFFCGE	YDSVVRTMTK
LIYV_RdRp	GTCFKLYEEM	MYKMFGFSP	LYDRDFKYTE	YFCRAKA.TC
CONSENSUS	--f-K-yE--	ly--fGfd-e	lld-----gE	Y---a-tl-- -l--sv--QR
	V		VI	
BYV_RdRp	KSGASNTWIG	NSIETLGILS	MFYYTNRFKA	LFVSGDDSLI
CTV_RdRp	RSGGSNTWIG	NSLVTLGILS	LYYDVSKFDL	LLVSGDDSLI
GLRaV3_RdRp	RSGGANTWLG	NSLVLCTLLS	VVLRGLDYSY	IVVSGDDSLI
LIYV_RdRp	RTGSPNTWLS	NTLVTLGMLL	SSYDIDDIDL	LLVSGDDSLI
CONSENSUS	rsG--NTW-G	Nslvtlg-ls	--y----f--	llVSGDDSLI fS-----n--
	VII		VIII	
BYV_RdRp	DAMCTELGFE	TKFLTPSPVY	FCSKFFVMTG	HDVFFVPDPY
CTV_RdRp	SEICLETGFE	TKFMSPSPVY	FCSKFVVQTG	NKTCFVPDPY
GLRaV3_RdRp	SVLSDNFGFD	VKIFNQAAPY	FCSKFLVQVE	DSLFFVPDPL
LIYV_RdRp	QEINKNFGME	AKYIEKSSPY	FCSKFIVELN	GKLKVIPDPI
CONSENSUS	-----fgfe	-Kf---s-PY	FCSKF-V---	----fvPDP- kl-vKlga--
BYV_RdRp	..KDEVDDDEF	LFEVFTSFRD	LTKDLVDERV	IELLTHLVHS
CTV_RdRp	..QNKLTDVE	LFELFTSFKD	MTQDFGDQVV	LEKLKLLVEA
GLRaV3_RdRp	..KTSIDID.L	LHEIFQSFDV	LSKGFNREDV	IQELAKLVTR
LIYV_RdRp	RQEDFVNGSV	VKERFISFKD	LMKEYDNDVA	VIRIDEAVCY
CONSENSUS	-----d--	l-E-F-SF-D	l-kdf--e-v	i--l--lv-- ky---sG-ty
BYV_RdRp	AALCAIH CIR	SNFSSFKKLY		
CTV_RdRp	PALCAIH CVR	SNFLSFERLF		
GLRaV3_RdRp	SALCVLHVLS	ANFSQFCRLY		
LIYV_RdRp	AALCYIHCCM	SNFVSFRRIY		
CONSENSUS	-ALC-iHc--	sNF-sF-rly		

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**FIG. 23**

**FIG. 24**

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transmembrane

1 54  
BYV\_p7K MDCVLRSYLL LAFGELICLF LFCLVFIWF VYKQILFRTT AQSNEARHNH STTV\*  
LIYV\_p5K ..... MSILFFL MSILVFIFF ILKLLFVNTD SEVNIPNKS R F\* ...  
GLRaV3\_p5K ..... MDD FKQAILLLV DFVFIILL VLTFFVPRLQ QSSTINTGLR TV\*..  
CTV\_p6K MDCVIQGLT FLVGIAVFA FAGLIIVIT IYRCTIKPVR SASPYGTHAT V\* ...  
CONSENSUS ----- f---il-f-- ---lvi-i-- -----S-----

FIG. 25



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FIG. 26A

A					
BYV_p65	..MVVFGLDF	GTTFSSVCAY	VGEELYLFKQ	RDSAYIPTV	FLHSDTQEVA
CTV_p65	..MVLLGLDF	GTTFSTVAMA	TPSELVILKQ	SNSSYIPTCL	LLHAEPNSVS
GLRaV3_p59	...MEVGIDF	GTTFSTICFS	PSGVSGCTPV	AGSVYVETQI	FIPEGSSSTYL
LIYV_p62	MRDCKVGLDF	GTTFSTVSTL	VNNSMYVLRL	GDSAYIPTCI	AITPGGEAI.
CONSENSUS	-----GIDF	GTTFStv---	----l--l--	--S-YipTci	f-----v-
BYV_p65	FGYDAEVLNS	DLSVRGGFYR	DLKRWIGCDE	ENYRDYLEKL	KPHYKTELLK
CTV_p65	YGYDAEYLAA	S.GESGSFYK	DLKRWVGCTA	KNYQTYLHKL	SPSYKVIVKE
GLRaV3_p59	IG.KAAGKAY	RDGVEGRLYV	NPKRWVGVTR	DNVERYVEKL	KPTYTVKM..
LIYV_p62	IGGAAEVLSG	DDTPHCFYF.	DLKRWVGVD	NTFKFAMNKI	RPKYVAELVE
CONSENSUS	-G--Ae-l--	-----g-fY-	dlKRWvG---	-ny--yl-Kl	-P-Y---l--
BYV_p65	VAQSSKSTVK	LDCYSGTVPQ	NATLPGLIAT	FVKALISTAS	EAFKCQCTGV
CTV_p65	FGTKSVVPY	LSPLNNDLGL	SVALPSLIAS	YAKSILSDAE	RVFNVSCTGV
GLRaV3_p59	...DSGGALL	IGGLSGPDT	LLRVVDVICL	FLRALILECE	RYTSTTVTAA
LIYV_p62	.....GEVY	LTGINKGFSI	KLSVKQLIKA	YIETIVRLLA	SSYSLRVIDL
CONSENSUS	----s-----	l-----	-----lI--	-----i----	--f----T--
B					
BYV_p65	ICSVPANYN	LQRSFTESC	NLSGYPCVYM	VNEPSAAALS	ACSRIKGATS
CTV_p65	ICSVPAGYNT	LQRAFTQQSI	MSGYSCVYI	INEPSAAAYS	TLPKLNADK
GLRaV3_p59	VVTVPADYNS	FKRSFVVEAL	KGLGIPVRGV	VNEPTAAALY	SLAKSRVEDL
LIYV_p62	NQSVPADYKN	AQRLAARSVL	KALSFPCRR	INEPSAAAVY	CVSRYPNYNY
CONSENSUS	i-sVPA-Yn-	lqR-f-----	---gypc--i	-NEPSAAA--	-----
C			D		
BYV_p65	PVLVYDFGGG	TFDVSVISAL	NNTFVVRASG	GDMNLGGRDI	DKAFVEHLYN
CTV_p65	YLAVYDFGGG	TFDVSIVSVR	LPTFAVRSSS	GDMNLGGRDI	DKKLSDKIYE
GLRaV3_p59	LLAVDFDFGGG	TFDVSFVKKK	GNILCVIFSV	GDNFLGGRDI	DRAIVEVIKQ
LIYV_p62	FL.VYDFGGG	TFDVSIGKY	KSYVTVIDTE	GDSFLGGRDI	DKSIEDYLVG
CONSENSUS	-l-VyDFGGG	TFDVS-----	---f-V--s-	GD--LGGRDI	Dk-----
BYV_p65	KAQ...LPVN	YKIDISFLKE	SLSKKVSFLN	FPVSEQGVR	VDVLNVNSEL
CTV_p65	MAD...FVPQ	KELNVSSLKE	ALSLQTPVK	YT.VNHYGMS	ETVSIDQTVL
GLRaV3_p59	KIKGASDAK	LGIFVSSMKE	DLSNNNAITQ	HLIPVEGGVE	V.VDLTSDDEL
LIYV_p62	KYNIKKVIP.	.ATYLALIKE	E.CNNTNKS	FTILFDDGSV	QVVEFSKSEL
CONSENSUS	k-----	----vs-lKE	-ls-----	f-i--e-G--	--V-----eL
E					
BYV_p65	AEVAAPFVER	TIKIVKEVY.	.EKYCSSLRL	EPNVKAKLLM	VGGSSYLPGL
CTV_p65	REIASVFINR	TIDILTQV..	..KVKSSMPE	SQSL..KLVV	VGGSSYLPGL
GLRaV3_p59	DAIVAPFSAR	AVEVFKTGP.	.DNFYDPDVI	A.....VM	TGGSSALVKV
LIYV_p62	EKCVRPFVER	SIKLINDVVV	RNKLTSGV..	.....IYM	VGGSSLLQPV
CONSENSUS	--i--pFv-R	-i-i---v--	--k--s----	-----m	vGGSS-L---

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FIG. 26B

F

BYV_p65	LSRLSSIPFV	DEC.L.VLPD	ARAAVAGGCA	LYSACLRNDS	PMLLVDCAAH
CTV_p65	LDALATVPFV	SGI.V.PVED	ARTAVARGCA	LYSECLDGRS	KALLIDCITH
GLRaV3_p59	RSDVANLPQI	SKV.VFDSTD	FRCSVACGAK	VYCDTLAGNS	GLRLVDTLTN
LIYV_p62	QDMVRSYAST	KGLTLVADQD	MRSVSYGCS	VLHK.LEDNK	EIVYIDCNSH
CONSENSUS	-----p-v	-----D	-R-aVa-Gc-	-y---L---s	---l-Dc--h

G

BYV_p65	NLSISSKYCE	SIVCVPAAGSP	IPFTGVRTVN	MTGSNASAVY	SAALFEGDFV
CTV_p65	HLSVTTF SAD	SVVVAAAGSP	IPFEGERKLT	LRKCVSTS NY	QARMFEGDYE
GLRaV3_p59	TLTDEVVGLQ	PVVIFPKGSP	IPCSYTHRYT	V....GGGDV	VYGIFEGE..
LIYV_p62	PLSDISFNCD	PEPIIRKPMS	IPYHTTVKMR	HDRPLKT...	IVNIYEGSNL
CONSENSUS	-Ls-----d	-vvi---gsp	IPf-----	-----	----fEGd--

H

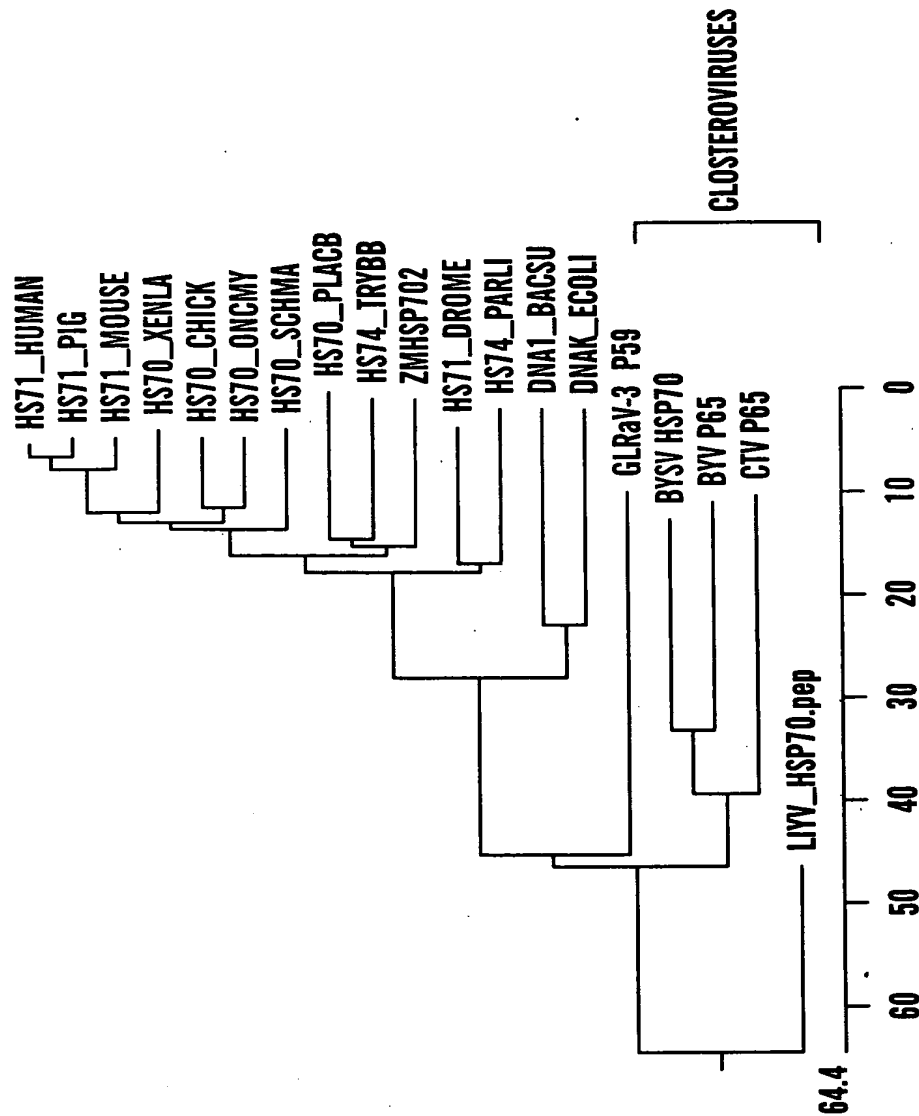
BYV_p65	KCRLNKRIFF	GDVVLGNVGV	TGSATRTVPL	TLEINVSSVG	TISFSLVGPT
CTV_p65	KVFRNERIYA	ASVSLFTLG V	NWSVPNDVEM	TLVTKVD SMG	KVEFY LKGPS
GLRaV3_p59	....NNRAFL	NEPTFRGVSK	RRGDPVETDV	A.QFN LSTDG	TVSVIVNGEE
LIYV_p62	FMPENDWLIS	SNINTTDFAK	.....VGEEY	SKVYEYDIDG	IITLKIRNEV
CONSENSUS	----N-r-f-	--v-l-----	-----e-	-----G	---f---g--

BYV_p65	GVKKLIGGNA	AYDFSSYQLG	ERVVADLHKH	NSDKVKLIHA	LTYQPFQRKK
CTV_p65	GELVNVQGTS	HYDYAGMPHP	TRKLVRLSDY	NVNSAALVLA	LTLTREKREK
GLRaV3_p59	VKNEYLVPGT	TNVLDSL...	...VYKSGRE	DLEAKA IPEY	LTTLNILHDK
LIYV_p62	TGKMFTLPNS	FTKSDNIKPI	TFKLTQLSNT	D.DLATLTSL	LGYHDKNFER
CONSENSUS	-----	-----	-----l---	--d---l---	Lt-----ek

BYV_p65	LTDGDKALFL	KRLTADYRRE	ARKFSSY...	.....DDAV	LNSSELLLGR
CTV_p65	FLLRT...LF	DTLLADLRKT	A.SLSEYSKK	YPITRNDIDV	VSSR...MGI
GLRaV3_p59	AFTRNLGNK	DKGFSDLRIE	ENFLKS....	...AVDTDTI	LNG*.....
LIYV_p62	FYG.....L	FNVPTILIKE	IDKLGGFKTL	YRRLKSMNAN	F.....
CONSENSUS	f-----l	-----dlr-e	---l--y---	-----v	l-----

BYV_p65	IIPKILRGSR	VEKLDV*
CTV_p65	VVSKVLRGSD	LERIPL.
GLRaV3_p59	.....	.....
LIYV_p62	.....	.....
CONSENSUS	-----	-----

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**FIG. 27**

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FIG. 28A

```

BYV_p61 MTTRFSTPAN YYWGELFRRF FGGQEW.... .KNLMSE AASVSRPRYS
CTV_p61 .....MSSH HVWGS�FRKF YGEAIW.... .KEYLSE STRNFDERNV
LIYV_P59 ..MLNDRIAV TCFQTLLKKS NVKHEMEQTN NYIVNNLADI NRNTFPALAG
GLRaV3_p55 .....MDK YIYVTGI..L NPNEARDEVF SVVNKGYIGP GGRSFSNRGS

```

CONSENSUS ----- --w--lf--f -----w---- ----k----- ----f--r--

```

BYV_p61 S.DFRFSDGV ILSRKTFGES TGES..FVRE FSLLLTFPKT YEVCKLCGVA
CTV_p61 SLDHTLSSGV VVRQSLNA PQGT..FENE LALLYNSVVI NDFVELTGMP
LIYV_P59 SVRIDFNSDY YISGGQIVVS PKDSNAYVKL LIVYLKYCYI N.YSAKTKYP
GLRaV3_p55 KYTVVWEN.. ..SAARISGL TSTSQSTIDA FAYFL..... ..LKGGLTTT

```

CONSENSUS s----f---- --s----- ---s--fv-- ---ll-----

```

BYV_p61 MELALNGMN. .RLSDYNVSE FN.....IV DVKTVGCKFN IQSVTEFVKK
CTV_p61 LKSLMTGIED RKVPD....E LI.....SV DPHEVGCRFT LNDVESYLMS
LIYV_P59 PQSLAVLDY DSFKAKWKY LDKSLTDYLD DNKTEGCSFT EQQVVEKYPQ
GLRaV3_p55 LSNPINCENW VRSSKDLSAF FRTLIKGIY ASRSVDSNLP KKDRDDIME.

```

CONSENSUS l---l----- ----- d---vgc-f- ---v-e---

```

BYV_p61 INGVAEPSL VEHCWSLSNS CGELINPKDT KRFVSLIFKG KDLAESTDEA
CTV_p61 RGEDFADLAA VEHSWCLNS CSRLLSSTEI DANKTLVF.T KNFDSNISG.
LIYV_P59 VDSLVAKIL. ....YRVCNS LGKLLDLKDF ENKNISGFEI NTAQDSPTVA
GLRaV3_p55 .ASRRLSPSD AAFCAVSVQ VGKYVDVTQN LESTIVPLRV MEIKKRRGSA

```

CONSENSUS -----a---- ----w--sns -g-l----d- -----f-- -----a

```

BYV_p61 IVS..SSYLD YLSHCLNLYE TCNLSSNSGK KSLYDEFLKH VIDYL...EN
CTV_p61 .VT..TKLET YLSYCISLYK KHCM.KDDDY FNLILPMFNC LMKVL...AS
LIYV_P59 DDN..ES.ND FFRECVDNR YYSSLSGSKL GKAKLEANAY IFKILLKSAS
GLRaV3_p55 HVSLPKVSA YVDFYTNLQE LLSDEVTRAR TDTVSAAYATD SMAFLVKMLP

```

CONSENSUS -v----- yl--c-nl-- ----- ----L-----

```

BYV_p61 SDLEYRSPSD NPLVAGILYD MCFEYNTLKS TYLKNIESFD CFLSLYLPLL
CTV_p61 LGLFYEKHAD NPLLTGMLIE FCLENKVYYS TFKVNLNVR LFKSKVLPV
LIYV_P59 GEFDIDRLSR NPLAISKFMN LYTNHVTDSE TFKSKFEALK SIKTPFASFI
GLRaV3_p55 LT.....AR EQWLKDVLYG LLVRRRPANF SYDVRVAWVY DVIATLKLVI

```

CONSENSUS --l----- npl----l-- lc----- t-----e--- -----i

```

BYV_p61 SEVFSMNWER PAPDVRLLE LDAAELLLKV PTINMHDST. ..FLYKNKLR
CTV_p61 LTVWDISEPD DPVDERVLIP FDPTDFVLDL PKLNIHDTM. ..VVVGNQIR
LIYV_P59 KKAFGIR... ..LN FEDSKIFYAL PKERQSDVLS DDMVESIVR
GLRaV3_p55 RLFFNKDTPG GIKDLKPCVP IESFDPFHES S..... ..SYFS

```

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FIG. 28B

BYV_p61	YLESYFEDDS	NELIKVKVDS	LLTRDNPEL.	.KLAQRWV..	...GFHCYYG
CTV_p61	QLEYVVESDA	LDDLSQHVDL	RLAADNPDL.	.RVGLRWA..	...GMFVYYG
LIYV_P59	DAASFTTVSD	NNYLPERVDR	FVTQLLLELF	PKTKASFPNK	IMFGFLHYFA
GLRaV3_p55	RLSYEMTTGK	GGKICPEIAE	KLVRRLMEEN	YKLRLT.PVM	ALIIILVYYS
CONSENSUS	-l-----	-----vd-	-l-----el-	-k----w---	---g-l-Yy-

II

BYV_p61	VFRTAQTRKV	KRDAEYKLPP	AL.....GE	FVINMSGVEE	FF.EELQKKM
CTV_p61	VYRCVVDRV	ERPTLFRLPQ	KLLSQDDGES	CSLHMGSVEA	LF.NLVQKVN
LIYV_P59	LSTTNSKR..	.....FNDTQ	ESTIEIEGET	LKISLKFITS	YLRNAIQSQH
GLRaV3_p55	IYGTNATRIK	RRPDFLNTRI	KGRVE.....	.KVSLRGVED	..RAFRISEK
CONSENSUS	vy-t---R--	-r---f----	-----	--i----ve-	-f----q---

BYV_p61	PSI...SVRR	RFCGSLSHEA	FSVFKRFGVG	FPPITRLNVP	VKYSYLNVDY
CTV_p61	KDI...NVR	QFMGRHSEVA	LRLYRNLGLR	FPPISSVRLP	AHHGYLYVDF
LIYV_P59	PDYADSNIVR	LWCNKRSNLA	LGYFKSRNIQ	LYLYS..KYP	RLLNYMRFDY
GLRaV3_p56	RGINAQRVLC	RYSDLTCLA	RRHYGIRRN	WKTLSYVD..	GTLAYDTADC
CONSENSUS	--i----v-r	-fc---s--A	l-----	f---s----p	----Yl--Dy

BYV_p61	YRHVKRVGLT	QDELTILSNI	EFDVAEMCCE	REVALQARRA	QR....GEKP
CTV_p61	YKRVPDGAVT	ADELESLRQL	RSSVDVMCKD	R.VSITPPPF	NRLRRGSSRT
LIYV_P59	FKGLDMGKLT	DEERLSIQTL	RCITEDRS.E	GTLATHNDLN	SWILRP....
GLRaV3_p55	ITSKVRNTIN	TADHASIIHY	IKTNENQVTG	TTLPHQL*..	.....
CONSENSUS	y-----t	-de--s----	----e----e	-----	-r-----

BYV_p61	FQGWKGTKNE	ISPHARSSIR	VKKNNDSLNN	ILWKDVGARS	QRRNLPLHRK
CTV_p61	FRGR.GARGA	SSRHMSRDVA	TSGFNLPYHG	RLYSTS*..	.....
LIYV_P59	.....	.....	.....	.....	.....
GLRaV3_p55	.....	.....	.....	.....	.....
CONSENSUS	-----	-----	-----	-----	-----

BYV_p61	H*
CTV_p61	..
LIYV_P59	..
GLRaV3_p55	..
CONSENSUS	--

(5' primer, 93-224)

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**FIG. 29A**

NcoI

tacttatctagaacc

ATGGAAGCGAGTCGACGACTA  
ATGGAAGCGAGTCGACGACTATCGCCATCGGACGCCGCTTTTGCAGAGCAGTGTGGTT  
9404-----+-----+-----+-----+-----+-----+-----+-----  
M E A S R R L S P S D A A F C R A V S V -  
CAGGTAGGGAAGTATGTGGACGTAACGCAGAATTTAGAAAGTACGATCGTGCCGTTAAGA  
-----+-----+-----+-----+-----+-----+-----+-----  
Q V G K Y V D V T Q N L E S T I V P L R -  
GTTATGGAAATAAAGAAAAGACGAGGATCAGCACATGTTAGTTTACCGAAGGTGGTATCC  
-----+-----+-----+-----+-----+-----+-----+-----  
V M E I K K R R G S A H V S L P K V V S -  
GCTTACGTAGATTTTTTATACGAACTTGCAGGAATTGCTGTCCGATGAAGTAACTAGGGCC  
-----+-----+-----+-----+-----+-----+-----+-----  
A Y V D F Y T N L Q E L L S D E V T R A -  
AGAACCGATACAGTTTCGGCATAACGCTACCGACTCTATGGCTTTCTTAGTTAAGATGTTA  
-----+-----+-----+-----+-----+-----+-----+-----  
R T D T V S A Y A T D S M A F L V K M L -  
CCCCTGACTGCTCGTGAGCAGTGGTTAAAAGACGTGCTAGGATATCTGCTGGTACGGAGA  
-----+-----+-----+-----+-----+-----+-----+-----  
P L T A R E Q W L K D V L G Y L L V R R -  
CGACCAGCAAATTTTTCCTACGACGTAAGAGTAGCTTGGGTATATGACGTGATCGCTACG  
-----+-----+-----+-----+-----+-----+-----+-----  
R P A N F S Y D V R V A W V Y D V I A T -  
CTCAAGCTGGTCATAAGATTGTTTTTCAACAAGGACACACCCGGGGGTATTAAAGACTTA  
-----+-----+-----+-----+-----+-----+-----+-----  
L K L V I R L F F N K D T P G G I K D L -  
AAACCGTGTGTGCCTATAGAGTCATTTCGACCCCTTTCACGAGCTTTCGTCCTATTTCTCT  
-----+-----+-----+-----+-----+-----+-----+-----  
K P C V P I E S F D P F H E L S S Y F S -  
AGGTAAAGTTACGAGATGACGACAGGTAAAGGGGAAAGATATGCCCCGAGATCGCCGAG  
-----+-----+-----+-----+-----+-----+-----+-----  
R L S Y E M T T G K G G K I C P E I A E -  
AAGTTGGTGCGCCGTCTAATGGAGGAAACTATAAGTTAAGATTGACCCCGAGTGATGGCC  
-----+-----+-----+-----+-----+-----+-----+-----  
K L V R R L M E E N Y K L R L T P V M A -

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**FIG. 29B**

TTAATAATTATACTGGTATACTACTCCATTTACGGCACAAACGCTACCAGGATTAAAAGA

-----+-----+-----+-----+-----+-----+-----+-----+-----+-----  
L I I I L V Y Y S I Y G T N A T R I K R -

CGCCCGGATTTCTCAATGTGAGGATAAAGGGAAGAGTCGAGAAGGTTTCGTTACGGGGG

-----+-----+-----+-----+-----+-----+-----+-----+-----+-----  
R P D F L N V R I K G R V E K V S L R G -

GTAGAAGATCGTGCCTTTAGAATATCAGAAAAGCGCGGGATAAACGCTCAACGTGTATTA

-----+-----+-----+-----+-----+-----+-----+-----+-----+-----  
V E D R A F R I S E K R G I N A Q R V L -

TGTAGGTACTATAGCGATCTCACATGTCTGGCTAGGCGACATTACGGCATTCGCAGGAAC

-----+-----+-----+-----+-----+-----+-----+-----+-----+-----  
C R Y Y S D L T C L A R R H Y G I R R N -

AATTGGAAGACGCTGAGTTATGTAGACGGGACGTTAGCGTATGACACGGCTGATTGTATA

-----+-----+-----+-----+-----+-----+-----+-----+-----+-----  
N W K T L S Y V D G T L A Y D T A D C I -

ACTTCTAAGGTGAGAAATACGATCAACACCGCAGATCACGCTAGCATTATACACTATATC

-----+-----+-----+-----+-----+-----+-----+-----+-----+-----  
T S K V R N T I N T A D H A S I I H Y I -

AAGACGAACGAAAACCAGGTTACCGGAACTACTCTACCACACCAGCTTTAAAGCTGCGTG

-----+-----+-----+-----+-----+-----+-----+-----+-----+-----  
K T N E N Q V T G T T L P H Q L \*

TAGTATGCGACGATGTTTCT

-----+-----+-----+-----+-----+-----+-----+-----+-----+-----  
10503

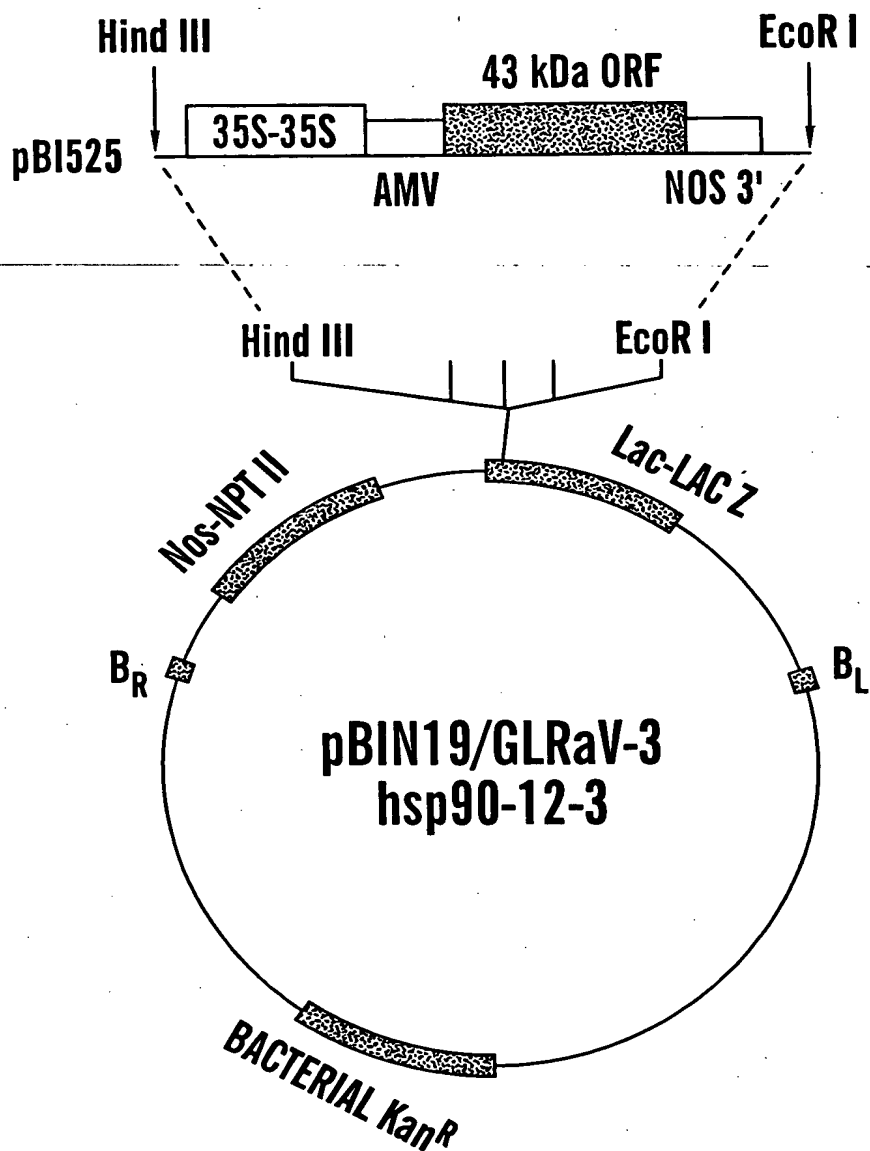
ATCATACGCTGCTACAAAGA

ggtacctaggagttct

NcoI

(3' primer, 93-225)

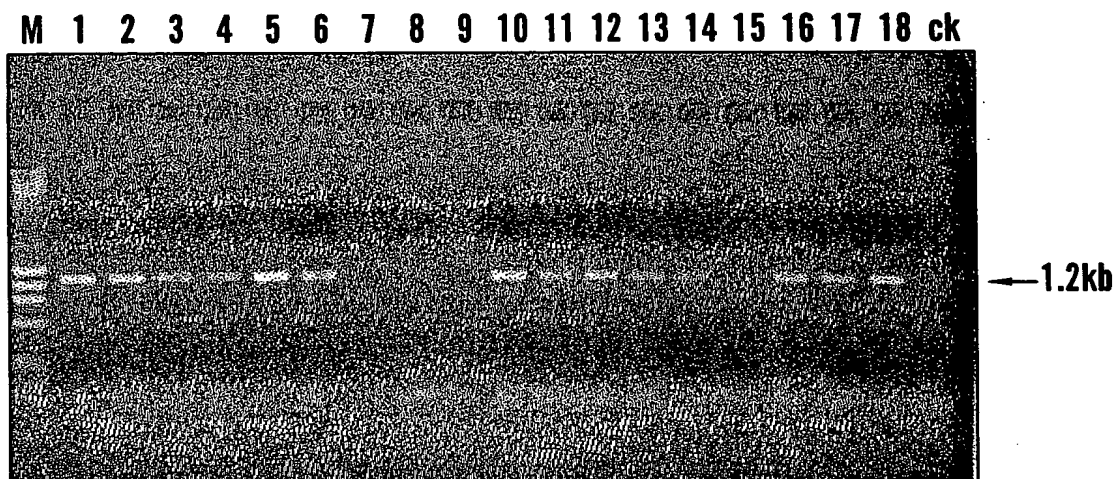
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**FIG. 30**

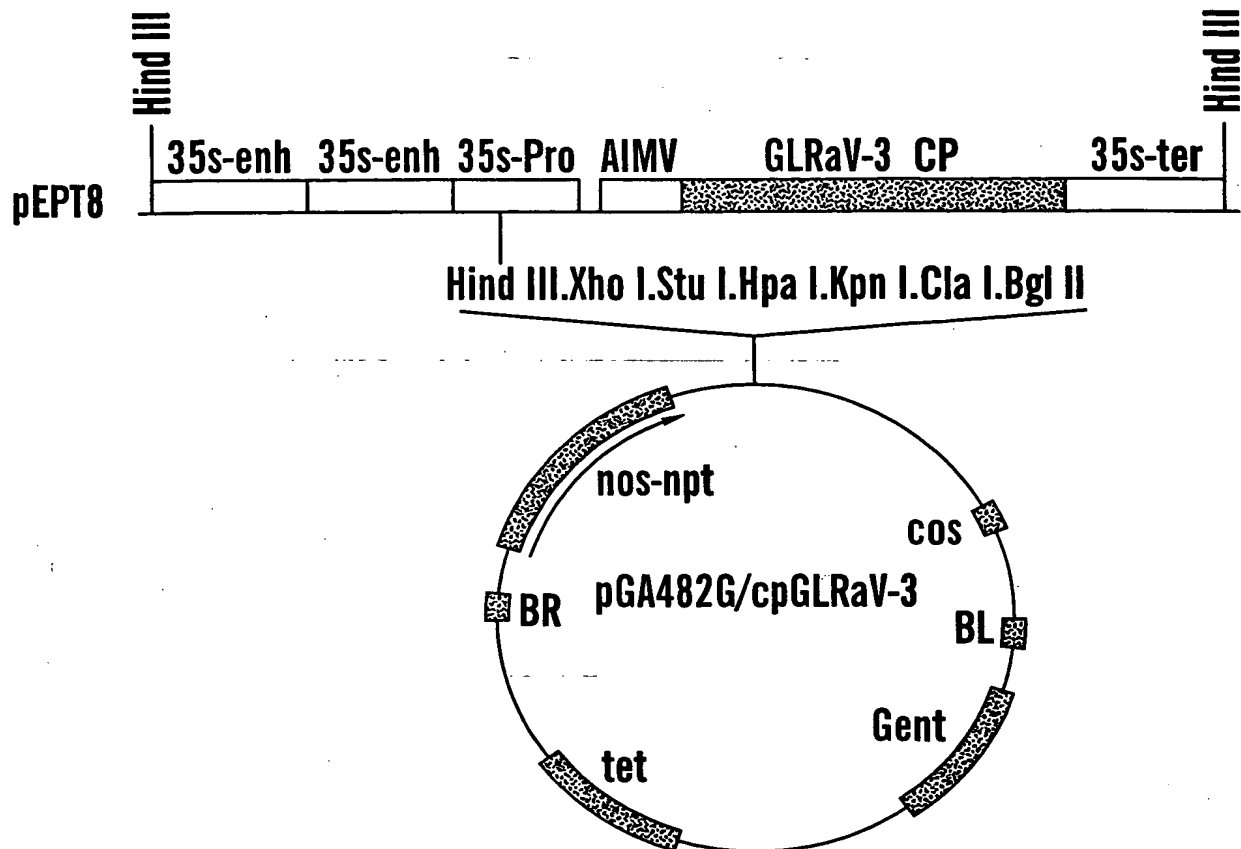


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***FIG. 31***

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**FIG. 32**